

SEQUENCE LISTING

Sequence No.: 1

Sequence length: 205

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Fibrosarcoma

Cell line: HT-1080

Clone name: HP00442

Sequence description

```

Met Thr Gly Leu Ala Leu Leu Tyr Ser Gly Val Phe Val Ala Phe Trp
 1              5              10              15
Ala Cys Ala Leu Ala Val Gly Val Cys Tyr Thr Ile Phe Asp Leu Gly
      20              25              30
Phe Arg Phe Asp Val Ala Trp Phe Leu Thr Glu Thr Ser Pro Phe Met
      35              40              45
Trp Ser Asn Leu Gly Ile Gly Leu Ala Ile Ser Leu Ser Val Val Gly
      50              55              60
Ala Ala Trp Gly Ile Tyr Ile Thr Gly Ser Ser Ile Ile Gly Gly Gly
      65              70              75              80
Val Lys Ala Pro Arg Ile Lys Thr Lys Asn Leu Val Ser Ile Ile Phe
      85              90              95
Cys Glu Ala Val Ala Ile Tyr Gly Ile Ile Met Ala Ile Val Ile Ser
      100             105             110
Asn Met Ala Glu Pro Phe Ser Ala Thr Asp Pro Lys Ala Ile Gly His
      115             120             125
Arg Asn Tyr His Ala Gly Tyr Ser Met Phe Gly Ala Gly Leu Thr Val
      130             135             140
Gly Leu Ser Asn Leu Phe Cys Gly Val Cys Val Gly Ile Val Gly Ser
      145             150             155             160
Gly Ala Ala Leu Ala Asp Ala Gln Asn Pro Ser Leu Phe Val Lys Ile
      165             170             175
Leu Ile Val Glu Ile Phe Gly Ser Ala Ile Gly Leu Phe Gly Val Ile
      180             185             190
Val Ala Ile Leu Gln Thr Ser Arg Val Lys Met Gly Asp
      195             200             205

```

Sequence No.: 2

Sequence length: 371

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Leukocyte

Clone name: HP00804

Sequence description

Met Ser His Glu Lys Ser Phe Leu Val Ser Gly Asp Asn Tyr Pro Pro
1 5 10 15
Pro Asn Pro Gly Tyr Pro Gly Gly Pro Gln Pro Pro Met Pro Pro Tyr
20 25 30
Ala Gln Pro Pro Tyr Pro Gly Ala Pro Tyr Pro Gln Pro Pro Phe Gln
35 40 45
Pro Ser Pro Tyr Gly Gln Pro Gly Tyr Pro His Gly Pro Ser Pro Tyr
50 55 60
Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Gly Gly Tyr Pro
65 70 75 80
Gln Gly Pro Tyr Pro Gln Glu Gly Tyr Pro Gln Gly Pro Tyr Pro Gln
85 90 95
Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Ser Pro Phe Pro Pro Asn
100 105 110
Pro Tyr Gly Gln Pro Gln Val Phe Pro Gly Gln Asp Pro Asp Ser Pro
115 120 125
Gln His Gly Asn Tyr Gln Glu Glu Gly Pro Pro Ser Tyr Tyr Asp Asn
130 135 140
Gln Asp Phe Pro Ala Thr Asn Trp Asp Asp Lys Ser Ile Arg Gln Ala
145 150 155 160
Phe Ile Arg Lys Val Phe Leu Val Leu Thr Leu Gln Leu Ser Val Thr
165 170 175
Leu Ser Thr Val Ser Val Phe Thr Phe Val Ala Glu Val Lys Gly Phe
180 185 190
Val Arg Glu Asn Val Trp Thr Tyr Tyr Val Ser Tyr Ala Val Phe Phe
195 200 205
Ile Ser Leu Ile Val Leu Ser Cys Cys Gly Asp Phe Arg Arg Lys His
210 215 220
Pro Trp Asn Leu Val Ala Leu Ser Val Leu Thr Ala Ser Leu Ser Tyr
225 230 235 240
Met Val Gly Met Ile Ala Ser Phe Tyr Asn Thr Glu Ala Val Ile Met
245 250 255

Ala Val Gly Ile Thr Thr Ala Val Cys Phe Thr Val Val Ile Phe Ser
 260 265 270
 Met Gln Thr Arg Tyr Asp Phe Thr Ser Cys Met Gly Val Leu Leu Val
 275 280 285
 Ser Met Val Val Leu Phe Ile Phe Ala Ile Leu Cys Ile Phe Ile Arg
 290 295 300
 Asn Arg Ile Leu Glu Ile Val Tyr Ala Ser Leu Gly Ala Leu Leu Phe
 305 310 315 320
 Thr Cys Phe Leu Ala Val Asp Thr Gln Leu Leu Gly Asn Lys Gln
 325 330 335
 Leu Ser Leu Ser Pro Glu Glu Tyr Val Phe Ala Ala Leu Asn Leu Tyr
 340 345 350
 Thr Asp Ile Ile Asn Ile Phe Leu Tyr Ile Leu Thr Ile Ile Gly Arg
 355 360 365
 Ala Lys Glu
 370

Sequence No.: 3

Sequence length: 179

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Stomach cancer

Clone name: HP01098

Sequence description

Met Leu Ser Leu Asp Phe Leu Asp Asp Val Arg Arg Met Asn Lys Arg
 1 5 10 15
 Gln Leu Tyr Tyr Gln Val Leu Asn Phe Gly Met Ile Val Ser Ser Ala
 20 25 30
 Leu Met Ile Trp Lys Gly Leu Met Val Ile Thr Gly Ser Glu Ser Pro
 35 40 45
 Ile Val Val Val Leu Ser Gly Ser Met Glu Pro Ala Phe His Arg Gly
 50 55 60
 Asp Leu Leu Phe Leu Thr Asn Arg Val Glu Asp Pro Ile Arg Val Gly
 65 70 75 80
 Glu Ile Val Val Phe Arg Ile Glu Gly Arg Glu Ile Pro Ile Val His
 85 90 95
 Arg Val Leu Lys Ile His Glu Lys Gln Asn Gly His Ile Lys Phe Leu
 100 105 110

95

Thr Lys Gly Asp Asn Asn Ala Val Asp Asp Arg Gly Leu Tyr Lys Gln
 115 120 125
 Gly Gln His Trp Leu Glu Lys Lys Asp Val Val Gly Arg Ala Arg Gly
 130 135 140
 Phe Val Pro Tyr Ile Gly Ile Val Thr Ile Leu Met Asn Asp Tyr Pro
 145 150 155 160
 Lys Phe Lys Tyr Ala Val Leu Phe Leu Leu Gly Leu Phe Val Leu Val
 165 170 175
 His Arg Glu

Sequence No.: 4

Sequence length: 347

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Liver

Clone name: HP01148

Sequence description

Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly
 1 5 10 15
 Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg
 20 25 30
 Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val
 35 40 45
 Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu
 50 55 60
 Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu
 65 70 75 80
 Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys
 85 90 95
 Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr
 100 105 110
 Asp Cys Ser His Glu Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu
 115 120 125
 Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro
 130 135 140
 Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr
 145 150 155 160
 Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys

96

165 170 175
 Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn
 180 185 190
 Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys
 195 200 205
 Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly
 210 215 220
 Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp
 225 230 235 240
 Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg
 245 250 255
 Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn
 260 265 270
 Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly
 275 280 285
 Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly
 290 295 300
 Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln
 305 310 315 320
 Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr
 325 330 335
 His Gln Glu Asp Val Ala Val Ile Cys Ser Gly
 340 345

Sequence No.: 5

Sequence length: 554

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Liver

Clone name: HP01293

Sequence description

Met Pro Thr Val Asp Asp Ile Leu Glu Gln Val Gly Glu Ser Gly Trp
 1 5 10 15
 Phe Gln Lys Gln Ala Phe Leu Ile Leu Cys Leu Leu Ser Ala Ala Phe
 20 25 30
 Ala Pro Ile Cys Val Gly Ile Val Phe Leu Gly Phe Thr Pro Asp His
 35 40 45
 His Cys Gln Ser Pro Gly Val Ala Glu Leu Ser Gln Arg Cys Gly Trp

50	55	60
Ser Pro Ala Glu Glu Leu Asn Tyr Thr Val Pro Gly Leu Gly Pro Ala		
65	70	75
Gly Glu Ala Phe Leu Gly Gln Cys Arg Arg Tyr Glu Val Asp Trp Asn		80
85	90	95
Gln Ser Ala Leu Ser Cys Val Asp Pro Leu Ala Ser Leu Ala Thr Asn		
100	105	110
Arg Ser His Leu Pro Leu Gly Pro Cys Gln Asp Gly Trp Val Tyr Asp		
115	120	125
Thr Pro Gly Ser Ser Ile Val Thr Glu Phe Asn Leu Val Cys Ala Asp		
130	135	140
Ser Trp Lys Leu Asp Leu Phe Gln Ser Cys Leu Asn Ala Gly Phe Phe		
145	150	155
Phe Gly Ser Leu Gly Val Gly Tyr Phe Ala Asp Arg Phe Gly Arg Lys		
165	170	175
Leu Cys Leu Leu Gly Thr Val Leu Val Asn Ala Val Ser Gly Val Leu		
180	185	190
Met Ala Phe Ser Pro Asn Tyr Met Ser Met Leu Leu Phe Arg Leu Leu		
195	200	205
Gln Gly Leu Val Ser Lys Gly Asn Trp Met Ala Gly Tyr Thr Leu Ile		
210	215	220
Thr Glu Phe Val Gly Ser Gly Ser Arg Arg Thr Val Ala Ile Met Tyr		
225	230	235
Gln Met Ala Phe Thr Val Gly Leu Val Ala Leu Thr Gly Leu Ala Tyr		
245	250	255
Ala Leu Pro His Trp Arg Trp Leu Gln Leu Ala Val Ser Leu Pro Thr		
260	265	270
Phe Leu Phe Leu Leu Tyr Tyr Trp Cys Val Pro Glu Ser Pro Arg Trp		
275	280	285
Leu Leu Ser Gln Lys Arg Asn Thr Glu Ala Ile Lys Ile Met Asp His		
290	295	300
Ile Ala Gln Lys Asn Gly Lys Leu Pro Pro Ala Asp Leu Lys Met Leu		
305	310	315
Ser Leu Glu Glu Asp Val Thr Glu Lys Leu Ser Pro Ser Phe Ala Asp		
325	330	335
Leu Phe Arg Thr Pro Arg Leu Arg Lys Arg Thr Phe Ile Leu Met Tyr		
340	345	350
Leu Trp Phe Thr Asp Ser Val Leu Tyr Gln Gly Leu Ile Leu His Met		
355	360	365
Gly Ala Thr Ser Gly Asn Leu Tyr Leu Asp Phe Leu Tyr Ser Ala Leu		
370	375	380
Val Glu Ile Pro Gly Ala Phe Ile Ala Leu Ile Thr Ile Asp Arg Val		
385	390	395
Gly Arg Ile Tyr Pro Met Ala Val Ser Asn Leu Leu Ala Gly Ala Ala		

98

405 410 415
 Cys Leu Val Met Ile Phe Ile Ser Pro Asp Leu His Trp Leu Asn Ile
 420 425 430
 Ile Ile Met Cys Val Gly Arg Met Gly Ile Thr Ile Ala Ile Gln Met
 435 440 445
 Ile Cys Leu Val Asn Ala Glu Leu Tyr Pro Thr Phe Val Arg Asn Leu
 450 455 460
 Gly Val Met Val Cys Ser Ser Leu Cys Asp Ile Gly Gly Ile Ile Thr
 465 470 475 480
 Pro Phe Ile Val Phe Arg Leu Arg Glu Val Trp Gln Ala Leu Pro Leu
 485 490 495
 Ile Leu Phe Ala Val Leu Gly Leu Leu Ala Ala Gly Val Thr Leu Leu
 500 505 510
 Leu Pro Glu Thr Lys Gly Val Ala Leu Pro Glu Thr Met Lys Asp Ala
 515 520 525
 Glu Asn Leu Gly Arg Lys Ala Lys Pro Lys Glu Asn Thr Ile Tyr Leu
 530 535 540
 Lys Val Gln Thr Ser Glu Pro Ser Gly Thr
 545 550

Sequence No.: 6

Sequence length: 350

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Epidermoid carcinoma

Cell line: KB

Clone name: HP10013

Sequence description

Met Ala Val Phe Val Val Leu Leu Ala Leu Val Ala Gly Val Leu Gly
 1 5 10 15
 Asn Glu Phe Ser Ile Leu Lys Ser Pro Gly Ser Val Val Phe Arg Asn
 20 25 30
 Gly Asn Trp Pro Ile Pro Gly Glu Arg Ile Pro Asp Val Ala Ala Leu
 35 40 45
 Ser Met Gly Phe Ser Val Lys Glu Asp Leu Ser Trp Pro Gly Leu Ala
 50 55 60
 Val Gly Asn Leu Phe His Arg Pro Arg Ala Thr Val Met Val Met Val
 65 70 75 80

Lys Gly Val Asn Lys Leu Ala Leu Pro Pro Gly Ser Val Ile Ser Tyr
 85 90 95
 Pro Leu Glu Asn Ala Val Pro Phe Ser Leu Asp Ser Val Ala Asn Ser
 100 105 110
 Ile His Ser Leu Phe Ser Glu Glu Thr Pro Val Val Leu Gln Leu Ala
 115 120 125
 Pro Ser Glu Glu Arg Val Tyr Met Val Gly Lys Ala Asn Ser Val Phe
 130 135 140
 Glu Asp Leu Ser Val Thr Leu Arg Gln Leu Arg Asn Arg Leu Phe Gln
 145 150 155 160
 Glu Asn Ser Val Leu Ser Ser Leu Pro Leu Asn Ser Leu Ser Arg Asn
 165 170 175
 Asn Glu Val Asp Leu Leu Phe Leu Ser Glu Leu Gln Val Leu His Asp
 180 185 190
 Ile Ser Ser Leu Leu Ser Arg His Lys His Leu Ala Lys Asp His Ser
 195 200 205
 Pro Asp Leu Tyr Ser Leu Glu Leu Ala Gly Leu Asp Glu Ile Gly Lys
 210 215 220
 Arg Tyr Gly Glu Asp Ser Glu Gln Phe Arg Asp Ala Ser Lys Ile Leu
 225 230 235 240
 Val Asp Ala Leu Gln Lys Phe Ala Asp Asp Met Tyr Ser Leu Tyr Gly
 245 250 255
 Gly Asn Ala Val Val Glu Leu Val Thr Val Lys Ser Phe Asp Thr Ser
 260 265 270
 Leu Ile Arg Lys Thr Arg Thr Ile Leu Glu Ala Lys Gln Ala Lys Asn
 275 280 285
 Pro Ala Ser Pro Tyr Asn Leu Ala Tyr Lys Tyr Asn Phe Glu Tyr Ser
 290 295 300
 Val Val Phe Asn Met Val Leu Trp Ile Met Ile Ala Leu Ala Leu Ala
 305 310 315 320
 Val Ile Ile Thr Ser Tyr Asn Ile Trp Asn Met Asp Pro Gly Tyr Asp
 325 330 335
 Ser Ile Ile Tyr Arg Met Thr Asn Gln Lys Ile Arg Met Asp
 340 345 350

Sequence No.: 7

Sequence length: 209

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

100

Cell kind: Fibrosarcoma

Cell line: HT-1080

Clone name: HP10034

Sequence description

```

Met Val Ser Ser Pro Cys Thr Gln Ala Ser Ser Arg Thr Cys Ser Arg
 1              5              10              15
Ile Leu Gly Leu Ser Leu Gly Thr Ala Ala Leu Phe Ala Ala Gly Ala
      20              25              30
Asn Val Ala Leu Leu Leu Pro Asn Trp Asp Val Thr Tyr Leu Leu Arg
      35              40              45
Gly Leu Leu Gly Arg His Ala Met Leu Gly Thr Gly Leu Trp Gly Gly
      50              55              60
Gly Leu Met Val Leu Thr Ala Ala Ile Leu Ile Ser Leu Met Gly Trp
      65              70              75              80
Arg Tyr Gly Cys Phe Ser Lys Ser Gly Leu Cys Arg Ser Val Leu Thr
      85              90              95
Ala Leu Leu Ser Gly Gly Leu Ala Leu Leu Gly Ala Leu Ile Cys Phe
      100             105             110
Val Thr Ser Gly Val Ala Leu Lys Asp Gly Pro Phe Cys Met Phe Asp
      115             120             125
Val Ser Ser Phe Asn Gln Thr Gln Ala Trp Lys Tyr Gly Tyr Pro Phe
      130             135             140
Lys Asp Leu His Ser Arg Asn Tyr Leu Tyr Asp Arg Ser Leu Trp Asn
      145             150             155             160
Ser Val Cys Leu Glu Pro Ser Ala Ala Val Val Trp His Val Ser Leu
      165             170             175
Phe Ser Ala Leu Leu Cys Ile Ser Leu Leu Gln Leu Leu Leu Val Val
      180             185             190
Val His Val Ile Asn Ser Leu Leu Gly Leu Phe Cys Ser Leu Cys Glu
      195             200             205

```

Lys

Sequence No.: 8

Sequence length: 163

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Fibrosarcoma

Cell line: HT-1080

101

Clone name: HP10050

Sequence description

```

Met Ala Ala Gly Leu Phe Gly Leu Ser Ala Arg Arg Leu Leu Ala Ala
 1           5           10           15
Ala Ala Thr Arg Gly Leu Pro Ala Ala Arg Val Arg Trp Glu Ser Ser
      20           25           30
Phe Ser Arg Thr Val Val Ala Pro Ser Ala Val Ala Gly Lys Arg Pro
      35           40           45
Pro Glu Pro Thr Thr Pro Trp Gln Glu Asp Pro Glu Pro Glu Asp Glu
      50           55           60
Asn Leu Tyr Glu Lys Asn Pro Asp Ser His Gly Tyr Asp Lys Asp Pro
      65           70           75           80
Val Leu Asp Val Trp Asn Met Arg Leu Val Phe Phe Phe Gly Val Ser
      85           90           95
Ile Ile Leu Val Leu Gly Ser Thr Phe Val Ala Tyr Leu Pro Asp Tyr
      100          105          110
Arg Cys Thr Gly Cys Pro Arg Ala Trp Asp Gly Met Lys Glu Trp Ser
      115          120          125
Arg Arg Glu Ala Glu Arg Leu Val Lys Tyr Arg Glu Ala Asn Gly Leu
      130          135          140
Pro Ile Met Glu Ser Asn Cys Phe Asp Pro Ser Lys Ile Gln Leu Pro
      145          150          155          160
Glu Asp Glu

```

Sequence No.: 9

Sequence length: 92

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Stomach cancer

Clone name: HP10071

Sequence description

```

Met Thr Lys Leu Ala Gln Trp Leu Trp Gly Leu Ala Ile Leu Gly Ser
 1           5           10           15
Thr Trp Val Ala Leu Thr Thr Gly Ala Leu Gly Leu Glu Leu Pro Leu
      20           25           30
Ser Cys Gln Glu Val Leu Trp Pro Leu Pro Ala Tyr Leu Leu Val Ser
      35           40           45

```

Sequence No. : 10

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Lymphoma

Cell line: U937

Clone name: HP10076

Sequence description

Met	Glu	Tyr	Leu	Ala	His	Pro	Ser	Thr	Leu	Gly	Leu	Ala	Val	Gly	Val
1				5					10					15	
Ala	Cys	Gly	Met	Cys	Leu	Gly	Trp	Ser	Leu	Arg	Val	Cys	Phe	Gly	Met
			20					25				30			
Leu	Pro	Lys	Ser	Lys	Thr	Ser	Lys	Thr	His	Thr	Asp	Thr	Glu	Ser	Glu
		35					40					45			
Ala	Ser	Ile	Leu	Gly	Asp	Ser	Gly	Glu	Tyr	Lys	Met	Ile	Leu	Val	Val
	50					55					60				
Arg	Asn	Asp	Leu	Lys	Met	Gly	Lys	Gly	Lys	Val	Ala	Ala	Gln	Cys	Ser
	65				70					75					80
His	Ala	Ala	Val	Ser	Ala	Tyr	Lys	Gln	Ile	Gln	Arg	Arg	Asn	Pro	Glu
			85						90					95	
Met	Leu	Lys	Gln	Trp	Glu	Tyr	Cys	Gly	Gln	Pro	Lys	Val	Val	Val	Lys
			100					105					110		
Ala	Pro	Asp	Glu	Glu	Thr	Leu	Ile	Ala	Leu	Leu	Ala	His	Ala	Lys	Met
		115					120					125			
Leu	Gly	Leu	Thr	Val	Ser	Leu	Ile	Gln	Asp	Ala	Gly	Arg	Thr	Gln	Ile
	130					135					140				
Ala	Pro	Gly	Ser	Gln	Thr	Val	Leu	Gly	Ile	Gly	Pro	Gly	Pro	Ala	Asp
145					150					155					160
Leu	Ile	Asp	Lys	Val	Thr	Gly	His	Leu	Lys	Leu	Tyr				
			165						170						

Sequence No.: 11
 Sequence length: 149
 Sequence type: Amino acid
 Topology: Linear
 Sequence kind: Protein
 Hypothetical: No
 Original source:
 Organism species: *Homo sapiens*
 Cell kind: Lymphoma
 Cell line: U937
 Clone name: HP10085
 Sequence description

Met	Met	Thr	Lys	His	Lys	Lys	Cys	Phe	Ile	Ile	Val	Gly	Val	Leu	Ile	1	5	10	15
Thr	Thr	Asn	Ile	Ile	Thr	Leu	Ile	Val	Lys	Leu	Thr	Arg	Asp	Ser	Gln	20	25	30	
Ser	Leu	Cys	Pro	Tyr	Asp	Trp	Ile	Gly	Phe	Gln	Asn	Lys	Cys	Tyr	Tyr	35	40	45	
Phe	Ser	Lys	Glu	Glu	Gly	Asp	Trp	Asn	Ser	Ser	Lys	Tyr	Asn	Cys	Ser	50	55	60	
Thr	Gln	His	Ala	Asp	Leu	Thr	Ile	Ile	Asp	Asn	Ile	Glu	Glu	Met	Asn	65	70	75	80
Phe	Leu	Arg	Arg	Tyr	Lys	Cys	Ser	Ser	Asp	His	Trp	Ile	Gly	Leu	Lys	85	90	95	
Met	Ala	Lys	Asn	Arg	Thr	Gly	Gln	Trp	Val	Asp	Gly	Ala	Thr	Phe	Thr	100	105	110	
Lys	Ser	Phe	Gly	Met	Arg	Gly	Ser	Glu	Gly	Cys	Ala	Tyr	Leu	Ser	Asp	115	120	125	
Asp	Gly	Ala	Ala	Thr	Ala	Arg	Cys	Tyr	Thr	Glu	Arg	Lys	Trp	Ile	Cys	130	135	140	
Arg	Lys	Arg	Ile	His	145														

Sequence No.: 12
 Sequence length: 188
 Sequence type: Amino acid
 Topology: Linear
 Sequence kind: Protein
 Hypothetical: No
 Original source:
 Organism species: *Homo sapiens*

Cell kind: Stomach cancer

Clone name: HP10122

Sequence description

```

Met Ser Thr Met Phe Ala Asp Thr Leu Leu Ile Val Phe Ile Ser Val
  1             5             10             15
Cys Thr Ala Leu Leu Ala Glu Gly Ile Thr Trp Val Leu Val Tyr Arg
          20             25             30
Thr Asp Lys Tyr Lys Arg Leu Lys Ala Glu Val Glu Lys Gln Ser Lys
      35             40             45
Lys Leu Glu Lys Lys Lys Glu Thr Ile Thr Glu Ser Ala Gly Arg Gln
      50             55             60
Gln Lys Lys Lys Ile Glu Arg Gln Glu Glu Lys Leu Lys Asn Asn Asn
      65             70             75             80
Arg Asp Leu Ser Met Val Arg Met Lys Ser Met Phe Ala Ile Gly Phe
          85             90             95
Cys Phe Thr Ala Leu Met Gly Met Phe Asn Ser Ile Phe Asp Gly Arg
          100             105             110
Val Val Ala Lys Leu Pro Phe Thr Pro Leu Ser Tyr Ile Gln Gly Leu
          115             120             125
Ser His Arg Asn Leu Leu Gly Asp Asp Thr Thr Asp Cys Ser Phe Ile
          130             135             140
Phe Leu Tyr Ile Leu Cys Thr Met Ser Ile Arg Gln Asn Ile Gln Lys
          145             150             155             160
Ile Leu Gly Leu Ala Pro Ser Arg Ala Ala Thr Lys Gln Ala Gly Gly
          165             170             175
Phe Leu Gly Pro Pro Pro Pro Ser Gly Lys Phe Ser
          180             185

```

Sequence No.: 13

Sequence length: 215

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Lymphoma

Cell line: U937

Clone name: HP10136

Sequence description

```

Met Val Leu Leu Thr Met Ile Ala Arg Val Ala Asp Gly Leu Pro Leu

```

105

1	5	10	15
Ala	Ala	Ser	Met
Gln	Glu	Asp	Glu
Gln	Ser	Gly	Arg
Asp	Leu	Gln	Gln
20	25	30	
Tyr	Gln	Ser	Gln
Ala	Lys	Gln	Leu
Phe	Arg	Lys	Leu
Asn	Glu	Gln	Ser
35	40	45	
Pro	Thr	Arg	Cys
Thr	Leu	Glu	Ala
Gly	Ala	Met	Thr
Phe	His	Tyr	Ile
50	55	60	
Ile	Glu	Gln	Gly
Val	Cys	Tyr	Leu
Val	Leu	Cys	Glu
Ala	Ala	Phe	Pro
65	70	75	80
Lys	Lys	Leu	Ala
Phe	Ala	Tyr	Leu
Glu	Asp	Leu	His
Ser	Glu	Phe	Asp
85	90	95	
Glu	Gln	His	Gly
Lys	Lys	Val	Pro
Thr	Val	Ser	Arg
Pro	Tyr	Ser	Phe
100	105	110	
Ile	Glu	Phe	Asp
Thr	Phe	Ile	Gln
Lys	Thr	Lys	Lys
Leu	Tyr	Ile	Asp
115	120	125	
Ser	Arg	Ala	Arg
Arg	Asn	Leu	Gly
Ser	Ile	Asn	Thr
Glu	Leu	Gln	Asp
130	135	140	
Val	Gln	Arg	Ile
Met	Val	Ala	Asn
Ile	Glu	Glu	Val
Leu	Gln	Arg	Gly
145	150	155	160
Glu	Ala	Leu	Ser
Ala	Leu	Asp	Ser
Lys	Ala	Asn	Asn
Leu	Ser	Ser	Leu
165	170	175	
Ser	Lys	Lys	Tyr
Arg	Gln	Asp	Ala
Lys	Tyr	Leu	Asn
Met	Arg	Ser	Thr
180	185	190	
Tyr	Ala	Lys	Leu
Ala	Ala	Val	Ala
Val	Phe	Phe	Ile
Met	Leu	Ile	Val
195	200	205	
Tyr	Val	Arg	Phe
Trp	Trp	Leu	
210	215		

Sequence No.: 14

Sequence length: 112

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Stomach cancer

Clone name: HP10175

Sequence description

Met	Gln	Asp	Thr	Gly	Ser	Val	Val	Pro	Leu	His	Trp	Phe	Gly	Phe	Gly
1	5	10	15												
Tyr	Ala	Ala	Leu	Val	Ala	Ser	Gly	Gly	Ile	Ile	Gly	Tyr	Val	Lys	Ala

106

	20		25		30										
Gly	Ser	Val	Pro	Ser	Leu	Ala	Ala	Gly	Leu	Leu	Phe	Gly	Ser	Leu	Ala
	35				40						45				
Gly	Leu	Gly	Ala	Tyr	Gln	Leu	Ser	Gln	Asp	Pro	Arg	Asn	Val	Trp	Val
	50				55				60						
Phe	Leu	Ala	Thr	Ser	Gly	Thr	Leu	Ala	Gly	Ile	Met	Gly	Met	Arg	Phe
	65				70				75				80		
Tyr	His	Ser	Gly	Lys	Phe	Met	Pro	Ala	Gly	Leu	Ile	Ala	Gly	Ala	Ser
			85				90						95		
Leu	Leu	Met	Val	Ala	Lys	Val	Gly	Val	Ser	Met	Phe	Asn	Arg	Pro	His
	100						105						110		

Sequence No.: 15

Sequence length: 114

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Epidermoid carcinoma

Cell line: KB

Clone name: HP10179

Sequence description

Met	Glu	Lys	Pro	Leu	Phe	Pro	Leu	Val	Pro	Leu	His	Trp	Phe	Gly	Phe
1				5					10					15	
Gly	Tyr	Thr	Ala	Leu	Val	Val	Ser	Gly	Gly	Ile	Val	Gly	Tyr	Val	Lys
	20						25					30			
Thr	Gly	Ser	Val	Pro	Ser	Leu	Ala	Ala	Gly	Leu	Leu	Phe	Gly	Ser	Leu
	35						40					45			
Ala	Gly	Leu	Gly	Ala	Tyr	Gln	Leu	Tyr	Gln	Asp	Pro	Arg	Asn	Val	Trp
	50					55				60					
Gly	Phe	Leu	Ala	Ala	Thr	Ser	Val	Thr	Phe	Val	Gly	Val	Met	Gly	Met
	65				70				75				80		
Arg	Ser	Tyr	Tyr	Tyr	Gly	Lys	Phe	Met	Pro	Val	Gly	Leu	Ile	Ala	Gly
			85				90					95			
Ala	Ser	Leu	Leu	Met	Ala	Ala	Lys	Val	Gly	Val	Arg	Met	Leu	Met	Thr
	100						105					110			

Ser Asp

Sequence No.: 16

Sequence length: 327

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Fibrosarcoma

Cell line: HT-1080

Clone name: HP10196

Sequence description

Met Ala Ala Ala Ala Ala Ala Ala Ala Thr Asn Gly Thr Gly Gly
1 5 10 15
Ser Ser Gly Met Glu Val Asp Ala Ala Val Val Pro Ser Val Met Ala
20 25 30
Cys Gly Val Thr Gly Ser Val Ser Val Ala Leu His Pro Leu Val Ile
35 40 45
Leu Asn Ile Ser Asp His Trp Ile Arg Met Arg Ser Gln Glu Gly Arg
50 55 60
Pro Val Gln Val Ile Gly Ala Leu Ile Gly Lys Gln Glu Gly Arg Asn
65 70 75 80
Ile Glu Val Met Asn Ser Phe Glu Leu Leu Ser His Thr Val Glu Glu
85 90 95
Lys Ile Ile Ile Asp Lys Glu Tyr Tyr Tyr Thr Lys Glu Glu Gln Phe
100 105 110
Lys Gln Val Phe Lys Glu Leu Glu Phe Leu Gly Trp Tyr Thr Thr Gly
115 120 125
Gly Pro Pro Asp Pro Ser Asp Ile His Val His Lys Gln Val Cys Glu
130 135 140
Ile Ile Glu Ser Pro Leu Phe Leu Lys Leu Asn Pro Met Thr Lys His
145 150 155 160
Thr Asp Leu Pro Val Ser Val Phe Glu Ser Val Ile Asp Ile Ile Asn
165 170 175
Gly Glu Ala Thr Met Leu Phe Ala Glu Leu Thr Tyr Thr Leu Ala Thr
180 185 190
Glu Glu Ala Glu Arg Ile Gly Val Asp His Val Ala Arg Met Thr Ala
195 200 205
Thr Gly Ser Gly Glu Asn Ser Thr Val Ala Glu His Leu Ile Ala Gln
210 215 220
His Ser Ala Ile Lys Met Leu His Ser Arg Val Lys Leu Ile Leu Glu
225 230 235 240
Tyr Val Lys Ala Ser Glu Ala Gly Glu Val Pro Phe Asn His Glu Ile
245 250 255

108

Leu Arg Glu Ala Tyr Ala Leu Cys His Cys Leu Pro Val Leu Ser Thr
 260 265 270
 Asp Lys Phe Lys Thr Asp Phe Tyr Asp Gln Cys Asn Asp Val Gly Leu
 275 280 285
 Met Ala Tyr Leu Gly Thr Ile Thr Lys Thr Cys Asn Thr Met Asn Gln
 290 295 300
 Phe Val Asn Lys Phe Asn Val Leu Tyr Asp Arg Gln Gly Ile Gly Arg
 305 310 315 320
 Arg Met Arg Gly Leu Phe Phe
 325

Sequence No.: 17

Sequence length: 373

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Fibrosarcoma

Cell line: HT-1080

Clone name: HP10235

Sequence description

Met Thr Leu Cys Ala Met Leu Pro Leu Leu Leu Phe Thr Tyr Leu Asn
 1 5 10 15
 Ser Phe Leu His Gln Arg Ile Pro Gln Ser Val Arg Ile Leu Gly Ser
 20 25 30
 Leu Val Ala Ile Leu Leu Val Phe Leu Ile Thr Ala Ile Leu Val Lys
 35 40 45
 Val Gln Leu Asp Ala Leu Pro Phe Phe Val Ile Thr Met Ile Lys Ile
 50 55 60
 Val Leu Ile Asn Ser Phe Gly Ala Ile Leu Gln Gly Ser Leu Phe Gly
 65 70 75 80
 Leu Ala Gly Leu Leu Pro Ala Ser Tyr Thr Ala Pro Ile Met Ser Gly
 85 90 95
 Gln Gly Leu Ala Gly Phe Phe Ala Ser Val Ala Met Ile Cys Ala Ile
 100 105 110
 Ala Ser Gly Ser Glu Leu Ser Glu Ser Ala Phe Gly Tyr Phe Ile Thr
 115 120 125
 Ala Cys Ala Val Ile Ile Leu Thr Ile Ile Cys Tyr Leu Gly Leu Pro
 130 135 140
 Arg Leu Glu Phe Tyr Arg Tyr Tyr Gln Gln Leu Lys Leu Glu Gly Pro

109

145	150	155	160
Gly Glu Gln Glu Thr Lys Leu Asp Leu Ile Ser Lys Gly Glu Glu Pro			
	165	170	175
Arg Ala Gly Lys Glu Glu Ser Gly Val Ser Val Ser Asn Ser Gln Pro			
	180	185	190
Thr Asn Glu Ser His Ser Ile Lys Ala Ile Leu Lys Asn Ile Ser Val			
	195	200	205
Leu Ala Phe Ser Val Cys Phe Ile Phe Thr Ile Thr Ile Gly Met Phe			
	210	215	220
Pro Ala Val Thr Val Glu Val Lys Ser Ser Ile Ala Gly Ser Ser Thr			
	225	230	235
Trp Glu Arg Tyr Phe Ile Pro Val Ser Cys Phe Leu Thr Phe Asn Ile			
	245	250	255
Phe Asp Trp Leu Gly Arg Ser Leu Thr Ala Val Phe Met Trp Pro Gly			
	260	265	270
Lys Asp Ser Arg Trp Leu Pro Ser Leu Val Leu Ala Arg Leu Val Phe			
	275	280	285
Val Pro Leu Leu Leu Leu Cys Asn Ile Lys Pro Arg Arg Tyr Leu Thr			
	290	295	300
Val Val Phe Glu His Asp Ala Trp Phe Ile Phe Phe Met Ala Ala Phe			
	305	310	315
Ala Phe Ser Asn Gly Tyr Leu Ala Ser Leu Cys Met Cys Phe Gly Pro			
	325	330	335
Lys Lys Val Lys Pro Ala Glu Ala Glu Thr Ala Gly Ala Ile Met Ala			
	340	345	350
Phe Phe Leu Cys Leu Gly Leu Ala Leu Gly Ala Val Phe Ser Phe Leu			
	355	360	365
Phe Arg Ala Ile Val			
	370		

Sequence No.: 18

Sequence length: 183

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Stomach cancer

Clone name: HP10297

Sequence description

110

Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro
 1 5 10 15
 Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile
 20 25 30
 Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val
 35 40 45
 Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val
 50 55 60
 Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr
 65 70 75 80
 Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu
 85 90 95
 Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val
 100 105 110
 Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn
 115 120 125
 Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ser
 130 135 140
 Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala
 145 150 155 160
 Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe
 165 170 175
 Asp Arg His Lys Met Leu Ser
 180

Sequence No.: 19

Sequence length: 116

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Stomach cancer

Clone name: HP10299

Sequence description

Met Ala Ser Thr Val Val Ala Val Gly Leu Thr Ile Ala Ala Ala Gly
 1 5 10 15
 Phe Ala Gly Arg Tyr Val Leu Gln Ala Met Lys His Met Glu Pro Gln
 20 25 30
 Val Lys Gln Val Phe Gln Ser Leu Pro Lys Ser Ala Phe Ser Gly Gly
 35 40 45

111

Tyr Tyr Arg Gly Gly Phe Glu Pro Lys Met Thr Lys Arg Glu Ala Ala
 50 55 60
 Leu Ile Leu Gly Val Ser Pro Thr Ala Asn Lys Gly Lys Ile Arg Asp
 65 70 75 80
 Ala His Arg Arg Ile Met Leu Leu Asn His Pro Asp Lys Gly Gly Ser
 85 90 95
 Pro Tyr Ile Ala Ala Lys Ile Asn Glu Ala Lys Asp Leu Leu Glu Gly
 100 105 110
 Gln Ala Lys Lys
 115

Sequence No.: 20

Sequence length: 152

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Epidermoid carcinoma

Cell line: KB

Clone name: HP10301

Sequence description

Met Ala Val Leu Ser Lys Glu Tyr Gly Phe Val Leu Leu Thr Gly Ala
 1 5 10 15
 Ala Ser Phe Ile Met Val Ala His Leu Ala Ile Asn Val Ser Lys Ala
 20 25 30
 Arg Lys Lys Tyr Lys Val Glu Tyr Pro Ile Met Tyr Ser Thr Asp Pro
 35 40 45
 Glu Asn Gly His Ile Phe Asn Cys Ile Gln Arg Ala His Gln Asn Thr
 50 55 60
 Leu Glu Val Tyr Pro Pro Phe Leu Phe Phe Leu Ala Val Gly Gly Val
 65 70 75 80
 Tyr His Pro Arg Ile Ala Ser Gly Leu Gly Leu Ala Trp Ile Val Gly
 85 90 95
 Arg Val Leu Tyr Ala Tyr Gly Tyr Tyr Thr Gly Glu Pro Ser Lys Arg
 100 105 110
 Ser Arg Gly Ala Leu Gly Ser Ile Ala Leu Leu Gly Leu Val Gly Thr
 115 120 125
 Thr Val Cys Ser Ala Phe Gln His Leu Gly Trp Val Lys Ser Gly Leu
 130 135 140
 Gly Ser Gly Pro Lys Cys Cys His

145

150

Sequence No.: 21

Sequence length: 559

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Liver

Clone name: HP10302

Sequence description

Met Ala Pro Thr Leu Gln Gln Ala Tyr Arg Arg Arg Trp Trp Met Ala
 1 5 10 15
 Cys Thr Ala Val Leu Glu Asn Leu Phe Phe Ser Ala Val Leu Leu Gly
 20 25 30
 Trp Gly Ser Leu Leu Ile Ile Leu Lys Asn Glu Gly Phe Tyr Ser Ser
 35 40 45
 Thr Cys Pro Ala Glu Ser Ser Thr Asn Thr Thr Gln Asp Glu Gln Arg
 50 55 60
 Arg Trp Pro Gly Cys Asp Gln Gln Asp Glu Met Leu Asn Leu Gly Phe
 65 70 75 80
 Thr Ile Gly Ser Phe Val Leu Ser Ala Thr Thr Leu Pro Leu Gly Ile
 85 90 95
 Leu Met Asp Arg Phe Gly Pro Arg Pro Val Arg Leu Val Gly Ser Ala
 100 105 110
 Cys Phe Thr Ala Ser Cys Thr Leu Met Ala Leu Ala Ser Arg Asp Val
 115 120 125
 Glu Ala Leu Ser Pro Leu Ile Phe Leu Ala Leu Ser Leu Asn Gly Phe
 130 135 140
 Gly Gly Ile Cys Leu Thr Phe Thr Ser Leu Thr Leu Pro Asn Met Phe
 145 150 155 160
 Gly Asn Leu Arg Ser Thr Leu Met Ala Leu Met Ile Gly Ser Tyr Ala
 165 170 175
 Ser Ser Ala Ile Thr Phe Pro Gly Ile Lys Leu Ile Tyr Asp Ala Gly
 180 185 190
 Val Ala Phe Val Val Ile Met Phe Thr Trp Ser Gly Leu Ala Cys Leu
 195 200 205
 Ile Phe Leu Asn Cys Thr Leu Asn Trp Pro Ile Glu Ala Phe Pro Ala
 210 215 220
 Pro Glu Glu Val Asn Tyr Thr Lys Lys Ile Lys Leu Ser Gly Leu Ala

113

225 230 235 240
 Leu Asp His Lys Val Thr Gly Asp Leu Phe Tyr Thr His Val Thr Thr
 245 250 255
 Met Gly Gln Arg Leu Ser Gln Lys Ala Pro Ser Leu Glu Asp Gly Ser
 260 265 270
 Asp Ala Phe Met Ser Pro Gln Asp Val Arg Gly Thr Ser Glu Asn Leu
 275 280 285
 Pro Glu Arg Ser Val Pro Leu Arg Lys Ser Leu Cys Ser Pro Thr Phe
 290 295 300
 Leu Trp Ser Leu Leu Thr Met Gly Met Thr Gln Leu Arg Ile Ile Phe
 305 310 315 320
 Tyr Met Ala Ala Val Asn Lys Met Leu Glu Tyr Leu Val Thr Gly Gly
 325 330 335
 Gln Glu His Glu Thr Asn Glu Gln Gln Gln Lys Val Ala Glu Thr Val
 340 345 350
 Gly Phe Tyr Ser Ser Val Phe Gly Ala Met Gln Leu Leu Cys Leu Leu
 355 360 365
 Thr Cys Pro Leu Ile Gly Tyr Ile Met Asp Trp Arg Ile Lys Asp Cys
 370 375 380
 Val Asp Ala Pro Thr Gln Gly Thr Val Leu Gly Asp Ala Arg Asp Gly
 385 390 395 400
 Val Ala Thr Lys Ser Ile Arg Pro Arg Tyr Cys Lys Ile Gln Lys Leu
 405 410 415
 Thr Asn Ala Ile Ser Ala Phe Thr Leu Thr Asn Leu Leu Leu Val Gly
 420 425 430
 Phe Gly Ile Thr Cys Leu Ile Asn Asn Leu His Leu Gln Phe Val Thr
 435 440 445
 Phe Val Leu His Thr Ile Val Arg Gly Phe Phe His Ser Ala Cys Gly
 450 455 460
 Ser Leu Tyr Ala Ala Val Phe Pro Ser Asn His Phe Gly Thr Leu Thr
 465 470 475 480
 Gly Leu Gln Ser Leu Ile Ser Ala Val Phe Ala Leu Leu Gln Gln Pro
 485 490 495
 Leu Phe Met Ala Met Val Gly Pro Leu Lys Gly Glu Pro Phe Trp Val
 500 505 510
 Asn Leu Gly Leu Leu Leu Phe Ser Leu Leu Gly Phe Leu Leu Pro Ser
 515 520 525
 Tyr Leu Phe Tyr Tyr Arg Ala Arg Leu Gln Gln Glu Tyr Ala Ala Asn
 530 535 540
 Gly Met Gly Pro Leu Lys Val Leu Ser Gly Ser Glu Val Thr Ala
 545 550 555

Sequence length: 330

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Osteosarcoma

Cell line: U-2 OS

Clone name: HP10304

Sequence description

Met Glu Gly Ala Pro Pro Gly Ser Leu Ala Leu Arg Leu Leu Leu Phe
1 5 10 15
Val Ala Leu Pro Ala Ser Gly Trp Leu Thr Thr Gly Ala Pro Glu Pro
20 25 30
Pro Pro Leu Ser Gly Ala Pro Gln Asp Gly Ile Arg Ile Asn Val Thr
35 40 45
Thr Leu Lys Asp Asp Gly Asp Ile Ser Lys Gln Gln Val Val Leu Asn
50 55 60
Ile Thr Tyr Glu Ser Gly Gln Val Tyr Val Asn Asp Leu Pro Val Asn
65 70 75 80
Ser Gly Val Thr Arg Ile Ser Cys Gln Thr Leu Ile Val Lys Asn Glu
85 90 95
Asn Leu Glu Asn Leu Glu Glu Lys Glu Tyr Phe Gly Ile Val Ser Val
100 105 110
Arg Ile Leu Val His Glu Trp Pro Met Thr Ser Gly Ser Ser Leu Gln
115 120 125
Leu Ile Val Ile Gln Glu Glu Val Val Glu Ile Asp Gly Lys Gln Val
130 135 140
Gln Gln Lys Asp Val Thr Glu Ile Asp Ile Leu Val Lys Asn Arg Gly
145 150 155 160
Val Leu Arg His Ser Asn Tyr Thr Leu Pro Leu Glu Glu Ser Met Leu
165 170 175
Tyr Ser Ile Ser Arg Asp Ser Asp Ile Leu Phe Thr Leu Pro Asn Leu
180 185 190
Ser Lys Lys Glu Ser Val Ser Ser Leu Gln Thr Thr Ser Gln Tyr Leu
195 200 205
Ile Arg Asn Val Glu Thr Thr Val Asp Glu Asp Val Leu Pro Gly Lys
210 215 220
Leu Pro Glu Thr Pro Leu Arg Ala Glu Pro Pro Ser Ser Tyr Lys Val
225 230 235 240
Met Cys Gln Trp Met Glu Lys Phe Arg Lys Asp Leu Cys Arg Phe Trp
245 250 255

115

Ser Asn Val Phe Pro Val Phe Phe Gln Phe Leu Asn Ile Met Val Val
 260 265 270
 Gly Ile Thr Gly Ala Ala Val Val Ile Thr Ile Leu Lys Val Phe Phe
 275 280 285
 Pro Val Ser Glu Tyr Lys Gly Ile Leu Gln Leu Asp Lys Val Asp Val
 290 295 300
 Ile Pro Val Thr Ala Ile Asn Leu Tyr Pro Asp Gly Pro Glu Lys Arg
 305 310 315 320
 Ala Glu Asn Leu Glu Asp Lys Thr Cys Ile
 325 330

Sequence No.: 23

Sequence length: 108

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Osteosarcoma

Cell line: HU-2 OS

Clone name: HP10305

Sequence description

Met Ser Leu Thr Ser Ser Ser Ser Val Arg Val Glu Trp Ile Ala Ala
 1 5 10 15
 Val Thr Ile Ala Ala Gly Thr Ala Ala Ile Gly Tyr Leu Ala Tyr Lys
 20 25 30
 Arg Phe Tyr Val Lys Asp His Arg Asn Lys Ala Met Ile Asn Leu His
 35 40 45
 Ile Gln Lys Asp Asn Pro Lys Ile Val His Ala Phe Asp Met Glu Asp
 50 55 60
 Leu Gly Asp Lys Ala Val Tyr Cys Arg Cys Trp Arg Ser Lys Lys Phe
 65 70 75 80
 Pro Phe Cys Asp Gly Ala His Thr Lys His Asn Glu Glu Thr Gly Asp
 85 90 95
 Asn Val Gly Pro Leu Ile Ile Lys Lys Lys Glu Thr
 100 105

Sequence No.: 24

Sequence length: 101

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Osteosarcoma

Cell line: U-2 OS

Clone name: HP10306

Sequence description

Met Asn Leu Glu Arg Val Ser Asn Glu Glu Lys Leu Asn Leu Cys Arg
1 5 10 15
Lys Tyr Tyr Leu Gly Gly Phe Ala Phe Leu Pro Phe Leu Trp Leu Val
20 25 30
Asn Ile Phe Trp Phe Phe Arg Glu Ala Phe Leu Val Pro Ala Tyr Thr
35 40 45
Glu Gln Ser Gln Ile Lys Gly Tyr Val Trp Arg Ser Ala Val Gly Phe
50 55 60
Leu Phe Trp Val Ile Val Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile
65 70 75 80
Tyr Arg Pro Arg Trp Gly Ala Leu Gly Asp Tyr Leu Ser Phe Thr Ile
85 90 95
Pro Leu Gly Thr Pro
100

Sequence No.: 25

Sequence length: 372

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Epidermoid carcinoma

Cell line: KB

Clone name: HP10328

Sequence description

Met Lys Tyr Leu Arg His Arg Arg Pro Asn Ala Thr Leu Ile Leu Ala
1 5 10 15
Ile Gly Ala Phe Thr Leu Leu Leu Phe Ser Leu Leu Val Ser Pro Pro
20 25 30
Thr Cys Lys Val Gln Glu Gln Pro Pro Ala Ile Pro Glu Ala Leu Ala

117

35 40 45
 Trp Pro Thr Pro Pro Thr Arg Pro Ala Pro Ala Pro Cys His Ala Asn
 50 55 60
 Thr Ser Met Val Thr His Pro Asp Phe Ala Thr Gln Pro Gln His Val
 65 70 75 80
 Gln Asn Phe Leu Leu Tyr Arg His Cys Arg His Phe Pro Leu Leu Gln
 85 90 95
 Asp Val Pro Pro Ser Lys Cys Ala Gln Pro Val Phe Leu Leu Leu Val
 100 105 110
 Ile Lys Ser Ser Pro Ser Asn Tyr Val Arg Arg Glu Leu Leu Arg Arg
 115 120 125
 Thr Trp Gly Arg Glu Arg Lys Val Arg Gly Leu Gln Leu Arg Leu Leu
 130 135 140
 Phe Leu Val Gly Thr Ala Ser Asn Pro His Glu Ala Arg Lys Val Asn
 145 150 155 160
 Arg Leu Leu Glu Leu Glu Ala Gln Thr His Gly Asp Ile Leu Gln Trp
 165 170 175
 Asp Phe His Asp Ser Phe Phe Asn Leu Thr Leu Lys Gln Val Leu Phe
 180 185 190
 Leu Gln Trp Gln Glu Thr Arg Cys Ala Asn Ala Ser Phe Val Leu Asn
 195 200 205
 Gly Asp Asp Asp Val Phe Ala His Thr Asp Asn Met Val Phe Tyr Leu
 210 215 220
 Gln Asp His Asp Pro Gly Arg His Leu Phe Val Gly Gln Leu Ile Gln
 225 230 235 240
 Asn Val Gly Pro Ile Arg Ala Phe Trp Ser Lys Tyr Tyr Val Pro Glu
 245 250 255
 Val Val Thr Gln Asn Glu Arg Tyr Pro Pro Tyr Cys Gly Gly Gly Gly
 260 265 270
 Phe Leu Leu Ser Arg Phe Thr Ala Ala Ala Leu Arg Arg Ala Ala His
 275 280 285
 Val Leu Asp Ile Phe Pro Ile Asp Asp Val Phe Leu Gly Met Cys Leu
 290 295 300
 Glu Leu Glu Gly Leu Lys Pro Ala Ser His Ser Gly Ile Arg Thr Ser
 305 310 315 320
 Gly Val Arg Ala Pro Ser Gln His Leu Ser Ser Phe Asp Pro Cys Phe
 325 330 335
 Tyr Arg Asp Leu Leu Leu Val His Arg Phe Leu Pro Tyr Glu Met Leu
 340 345 350
 Leu Met Trp Asp Ala Leu Asn Gln Pro Asn Leu Thr Cys Gly Asn Gln
 355 360 365
 Thr Gln Ile Tyr
 370

118

Sequence No.: 26
Sequence length: 615
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
Organism species: *Homo sapiens*
Cell kind: Fibrosarcoma
Cell line: HT-1080
Clone name: HP00442

Sequence description

ATGACGGGGC TAGCACTGCT CTACTCCGGG GTCTTCGTGG CCTTCTGGGC CTGCGCGCTG	60
GCCGTGGGAG TCTGCTACAC CATTTTTGAT TTGGGCTTCC GCTTTGATGT GGCATGGTTC	120
CTGACGGAGA CTTCGCCCTT CATGTGGTCC AACCTGGGCA TTGGCCTAGC TATCTCCCTG	180
TCTGTGGTTG GGGCAGCCTG GGGCATCTAT ATTACGGGCT CCTCCATCAT TGGTGGAGGA	240
GTGAAGGCCC CCAGGATCAA GACCAAGAAC CTGGTCAGCA TCATCTTCTG TGAGGCTGTG	300
GCCATCTACG GCATCATCAT GGCAATTGTC ATTAGCAACA TGGCTGAGCC TTTCACTGCC	360
ACAGACCCCA AGGCCATCGG CCATCGGAAC TACCATGCAG GCTACTCCAT GTTTGGGGCT	420
GGCCTCACCG TAGGCCTGTC TAACCTCTTC TGTGGAGTCT GCGTGGGCAT CGTGGGCAGT	480
GGGGCTGCCC TGGCCGATGC TCAGAACCCC AGCCTCTTTG TAAAGATTCT CATCGTGGAG	540
ATCTTTGGCA GCGCCATTGG CCTCTTTGGG GTCATCGTCC CAATTCTTCA GACCTCCAGA	600
GTGAAGATGG GTGAC	615

Sequence No.: 27
Sequence length: 1113
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
Organism species: *Homo sapiens*
Cell kind: Leukocyte
Clone name: HP00804

Sequence description

ATGTCCCATG AAAAGAGTTT TTTGGTGTCT GGGGACAACT ATCCTCCCCC CAACCCTGGA	60
TATCCGGGGG GGCCCCAGCC ACCCATGCCC CCCTATGCTC AGCCTCCCTA CCCTGGGGCC	120
CCTTACCCAC AGCCCCCTTT CCAGCCCTCC CCCTACGGTC AGCCAGGGTA CCCCCATGGC	180
CCCAGCCCCCT ACCCCCAAGG GGGCTACCCA CAGGGTCCCT ACCCCCAAGG GGGCTACCCA	240
CAGGGCCCCCT ACCACAAGA GGGCTACCCA CAGGGCCCCCT ACCCCCAAGG GGGCTACCCC	300

119

CAGGGGCCAT ATCCCCAGAG CCCCTTCCCC CCCAACCCT ATGGACAGCC ACAGGTCTTC 360
CCAGGACAAG ACCCTGACTC ACCCCAGCAT GGAACTACC AGGAGGAGGG TCCCCATCC 420
TACTATGACA ACCAGGACTT CCCTGCCACC AACTGGGATG ACAAGAGCAT CCGACAGGCC 480
TTCATCCGCA AGGTGTTCTT AGTGCTGACC TTGCAGCTGT CCGTGACCCT GTCCACGGTG 540
TCTGTGTTCA CTTTGTGTC GGAGGTGAAG GGCTTTGTCC GGGAGAATGT CTGGACCTAC 600
TATGTCTCCT ATGCTGTCTT CTTCACTCT CTCTCGTCC TCAGCTGTTG TGGGGACTTC 660
CGGCGAAAAG ACCCCTGGAA CCTTGTGCA CTGTCGGTCC TGACCGCCAG CCTGTCTGAC 720
ATGGTGGGGA TGATCGCCAG CTTCTACAAC ACCGAGGCAG TCATCATGGC CGTGGGCATC 780
ACCACAGCCG TCTGCTTCAC CGTCGTATC TTCTCCATGC AGACCCGCTA CGACTTCACC 840
TCATGCATGG GCGTGCTCCT GGTGAGCATG GTGGTGCTCT TCATCTTCGC CATTCTCTGC 900
ATCTTCATCC GGAACCGCAT CCTGGAGATC GTGTACGCCT CACTGGGCGC TCTGCTCTTC 960
ACCTGCTTCC TCGCAGTGGA CACCCAGCTG CTGCTGGGGA ACAAGCAGCT GTCCCTGAGC 1020
CCAGAAGAGT ATGTGTTTGC TCGCTGAAC CTGTACACAG ACATCATCAA CATCTTCCTG 1080
TACATCTCA CCATCATTGG CCGCGCCAAG GAG 1113

Sequence No.: 28

Sequence length: 537

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Stomach cancer

Clone name: HP01098

Sequence description

ATGCTGTCTC TAGACTTTTT GGACGATGTG CGGCGGATGA ACAAGCGGCA GCTCTATTAT 60
CAAGTCTTAA ATTTTGGAAT GATTGTCTCA TCGGCACTAA TGATCTGGAA GGGGTTAATG 120
GTAATAACTG GAAGTGAAG TCCGATTGTA GTGGTGCTCA GTGGCAGCAT GGAACCTGCA 180
TTTCATAGAG GAGATCTTCT CTTTCTAACA AATCGAGTTG AAGATCCCAT ACGAGTGGGA 240
GAAATTGTTG TTTTAGGAT AGAAGGAAGA GAGATTCCTA TAGTTCACCG AGTCTTGAAG 300
ATTCATGAAA AGCAAAATGG GCATATCAAG TTTTGGACCA AAGGAGATAA TAATGCGGTT 360
GATGACCGAG GCCTCTATAA ACAAGGACAA CATTGGCTAG AGAAAAAGA TGTGTGGGG 420
AGAGCCAGGG GATTGTCTT TATATTGGA ATTGTGACGA TCCTCATGAA TGACTATCCT 480
AAATTAAAGT ATGCAGTTCT CTTTTTGCTG GGTATTTCG TGCTGGTTCA TCGTGAG 537

Sequence No.: 29

Sequence length: 1041

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Liver

Clone name: HP01148

Sequence description

ATGGCTCTGC TATTCTCCTT GATCCTTGCC ATTTGCACCA GACCTGGATT CCTAGCGTCT 60
CCATCTGGAG TCGGCTGGT GGGGGCCTC CACCGCTGTG AAGGCGGGT GGAGGTGGAA 120
CAGAAAGGCC AGTGGGGCAC CGTGTGTGAT GACGGCTGGG ACATTAAGGA CGTGGCTGTG 180
TTGTGCCGGG AGCTGGGCTG TGGAGCTGCC AGCGGAACCC CTAGTGGTAT TTTGTATGAG 240
CCACCAGCAG AAAAAGAGCA AAAGGTCCTC ATCCAATCAG TCAGTTGCAC AGGAACAGAA 300
GATACATTGG CTCAGTGTGA GCAAGAAGAA GTTTATGATT GTTCACATGA AGAAGATGCT 360
GGGGCATCGT GTGAGAACCC AGAGAGCTCT TTCTCCCCAG TCCCAGAGGG TGTCAGGCTG 420
GCTGACGGCC CTGGGCATTG CAAGGGACGC GTGGAAGTGA AGCACCAGAA CCAGTGGTAT 480
ACCGTGTGCC AGACAGGCTG GAGCCTCCGG GCCGCAAAGG TGGTGTGCCG GCAGCTGGGA 540
TGTGGGAGGG CTGTACTGAC TCAAAAACGC TGCAACAAGC ATGCCTATGG CCGAAAACCC 600
ATCTGGCTGA GCCAGATGTC ATGCTCAGGA CGAGAAGCAA CCCTTCAGGA TTGCCCTTCT 660
GGGCCTTGGG GGAAGAACAC CTGCAACCAT GATGAAGACA CGTGGGTCGA ATGTGAAGAT 720
CCCTTTGACT TGAGACTAGT AGGAGGAGAC AACCTCTGCT CTGGGCGACT GGAGGTGCTG 780
CACAAGGGCG TATGGGGCTC TGTCTGTGAT GACAACTGGG GAGAAAAGGA GGACCAGGTG 840
GTATGCAAGC AACTGGGCTG TGGGAAGTCC CTCTCTCCCT CCTTCAGAGA CCGGAAATGC 900
TATGGCCCTG GGGTTGGCCG CATCTGGCTG GATAATGTTT GTTGCTCAGG GGAGGAGCAG 960
TCCCTGGAGC AGTGCCAGCA CAGATTTTGG GGGTTTCACG ACTGCACCCA CCAGGAAGAT 1020
GTGGCTGTCA TCTGCTCAGG A 1041

Sequence No.: 30

Sequence length: 1662

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Liver

Clone name: HP01293

Sequence description

ATGCCCACCG TGGATGACAT TCTGGAGCAG GTTGGGGAGT CTGGCTGGTT CCAGAAGCAA 60
GCCTTCTCA TCTTATGCCT GCTGTGGCT GCCTTTGCGC CCATCTGTGT GGGCATCGTC 120
TTCCTGGGTT TCACACCTGA CCACCACTGC CAGAGTCTG GGGTGGCTGA GCTGAGCCAG 180
CGCTGTGGCT GGAGCCCTGC GGAGGAGCTG AACTATACAG TGCCAGGCCT GGGGCCCCGC 240
GGCGAGGCCT TCCTTGGCCA GTGCAGGCGC TATGAAAGTGG ACTGGAACCA GAGCGCCCTC 300

121

```

AGCTGTGTAG ACCCCCTGGC TAGCCTGGCC ACCAACAGGA GCCACCTGCC GCTGGGTCCC 360
TGCCAGGATG GCTGGGTGTA TGACACGCCC GGCTCTTCCA TCGTCACTGA GTTCAACCTG 420
GTGTGTGCTG ACTCCTGGAA GCTGGACCTC TTTCAGTCCT GTTTGAATGC GGGCTTCTTC 480
TTTGGCTCTC TCGGTGTTGG CTACTTTGCA GACAGGTTTG GCCGTAAGCT GTGTCTCCTG 540
GGAAGTGTGC TGGTCAACGC GGTGTCGGGC GTGCTCATGG CCTTCTCGCC CAACTACATG 600
TCCATGCTGC TCTTCCGCCT GCTGCAGGGC CTGGTCAGCA AGGGCAACTG GATGGCTGGC 660
TACACCCTAA TCACAGAATT TGTGGCTCG GGCTCCAGAA GAACGGTGGC GATCATGTAC 720
CAGATGGCCT TCACGGTGGG GCTGGTGGCG CTTACCGGGC TGGCCTACGC CCTGCCTCAC 780
TGGCGCTGGC TGCAGCTGGC AGTCTCCCTG CCCACCTTCC TCTTCCTGCT CTACTACTGG 840
TGTGTGCCGG AGTCCCCTCG GTGGCTGTTA TCACAAAAAA GAAACACTGA AGCAATAAAG 900
ATAATGGACC ACATCGCTCA AAAGAATGGG AAGTTGCCTC CTGCTGATTT AAAGATGCTT 960
TCCCTCGAAG AGGATGTCAC CGAAAAGCTG AGCCCTTCAT TTGCAGACCT GTTCCGCACG 1020
CCGCGCCTGA GGAAGCGCAC CTTCATCCTG ATGTACCTGT GGTTCACGGA CTCTGTGCTC 1080
TATCAGGGGC TCATCCTGCA CATGGGCGCC ACCAGCGGGA ACCTCTACCT GGATTTCTTT 1140
TACTCCGCTC TGGTCGAAAT CCCGGGGGCC TTCATAGCCC TCATCACCAT TGACCGCGTG 1200
GGCCGCATCT ACCCCATGGC CGTGTCAAAT TTGTTGGCGG GGGCAGCCTG CCTCGTCATG 1260
ATTTTTATCT CACCTGACCT GCACTGGTTA AACATCATAA TCATGTGTGT TGGCCGAATG 1320
GGAATCACCA TTGCAATACA AATGATCTGC CTGGTGAATG CTGAGCTGTA CCCCACATTC 1380
GTCAGGAACC TCGGAGTGAT GGTGTGTTCC TCCCTGTGTG ACATAGGTGG GATAATCACC 1440
CCCTTCATAG TCTTCAGGCT GAGGGAGGTC TGGCAAGCCT TGCCCCTCAT TTTGTTTGGC 1500
GTGTTGGGCC TGCTTGCCGC GGGAGTGACG CTACTTCTTC CAGAGACCAA GGGGGTCGCT 1560
TTGCCAGAGA CCATGAAGGA CGCCGAGAAC CTTGGGAGAA AAGCAAAGCC CAAAGAAAAC 1620
ACGATTIACC TTAAGGTCCA AACCTCAGAA CCCTCGGGCA CC 1662

```

Sequence No.: 31

Sequence length: 1050

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Epidermoid carcinoma

Cell line: KB

Clone name: HP10013

Sequence description

```

ATGGCTGTGT TTGTCGTGCT CCTGGCGTTG GTGGCGGGTG TTTTGGGGAA CGAGTTTAGT 60
ATATTAAAAT CACCAGGGTC TGTGTTTTTC CGAAATGGAA ATTGGCCTAT ACCAGGAGAG 120
CGGATCCCAG ACGTGGCTGC ATTGTCCATG GGCTTCTCTG TGAAAGAAGA CCTTCTTGG 180
CCAGGACTCG CAGTGGGTAA CCTGTTTCAT CGTCCTCGGG CTACCGTCAT GGTGATGGTG 240
AAGGGAGTGA ACAAAGTGGC TCTACCCCCA GGCAGTGTCA TTTCGTACCC TTTGGAGAAT 300
GCAGTTCCTT TTAGTCTTGA CAGTGTGCA AATTCCATTC ACTCCTTATT TTCTGAGGAA 360

```

122

ACTCCTGTTG	TTTTGCAGTT	GGCTCCCAGT	GAGGAAAGAG	TGTATATGGT	AGGGAAGGCA	420
AACTCAGTGT	TTGAAGACCT	TTCAGTCACC	TTGCGCCAGC	TCCGTAATCG	CCTGTTTCAA	480
GAAAACTCTG	TTCTCAGTTC	ACTCCCCCTC	AATTCTCTGA	GTAGGAACAA	TGAAGTTGAC	540
CTGCTCTTTT	TTTCTGAACT	GCAAGTGCTA	CATGATATTT	CAAGCTTGCT	GTCTCGTCAT	600
AAGCATCTAG	CCAAGGATCA	TTCTCCTGAT	TTATATTAC	TGGAGCTGGC	AGGTTTGGAT	660
GAAATTGGGA	AGCGTTATGG	GGAAGACTCT	GAACAATTCA	GAGATGCTTC	TAAGATCCTT	720
GTTGACGCTC	TGCAAAAGTT	TGCAGATGAC	ATGTACAGTC	TTTATGGTGG	GAATGCAGTG	780
GTAGAGTTAG	TCACTGTCAA	GTCATTTGAC	ACCTCCCTCA	TTAGGAAGAC	AAGGACTATC	840
CTTGAGGCAA	AACAAGCGAA	GAACCCAGCA	AGTCCCTATA	ACCTTGCATA	TAAGTATAAT	900
TTTGAATATT	CCGTGGTTTT	CAACATGGTA	CTTTGGATAA	TGATCGCCTT	GGCCTTGGCT	960
GTGATTATCA	CCTCTTACAA	TATTTGGAAC	ATGGATCCTG	GATATGATAG	CATCATTTAT	1020
AGGATGACAA	ACCAGAAGAT	TCGAATGGAT				1050

Sequence No.: 32

Sequence length: 627

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Fibrosarcoma

Cell line: HT-1080

Clone name: HP10034

Sequence description

ATGGTGTCTT	CTCCCTGCAC	GCAGGCAAGC	TCACGGACTT	GCTCCCGTAT	CCTGGGACTG	60
AGCCTTGGGA	CTGCAGCCCT	GTTTGCTGCT	GGGGCCAACG	TGGCACTCCT	CCTTCCTAAC	120
TGGGATGTCA	CCTACCTGTT	GAGGGGCCTC	CTTGGCAGGC	ATGCCATGCT	GGGAAGTGGG	180
CTCTGGGGAG	GAGGCCTCAT	GGTACTCACT	GCAGCTATCC	TCATCTCCTT	GATGGGCTGG	240
AGATACGGCT	GCTTCAGTAA	GAGTGGGCTC	TGTCGAAGCG	TGCTTACTGC	TCTGTTGTCA	300
GGTGGCCTGG	CTTTACTTGG	AGCCCTGATT	TGCTTTGTCA	CTTCTGGAGT	TGCTCTGAAA	360
GATGGTCCTT	TTTGCATGTT	TGATGTTTCA	TCCTTCAATC	AGACACAAGC	TTGGAAATAT	420
GGTTACCCAT	TCAAAGACCT	GCATAGTAGG	AATTATCTGT	ATGACCGTTC	GCTCTGGAAC	480
TCCGTCTGCC	TGGAGCCCTC	TGCAGCTGTT	GTCTGGCAGC	TGTCCCTCTT	CTCCGCCCTT	540
CTGTGCATCA	GCCTGCTCCA	GCTTCTCCTG	GTGGTCGTTT	ATGTCATCAA	CAGCCTCCTG	600
GGCCTTTTCT	GCAGCCTCTG	CGAGAAG				627

Sequence No.: 33

Sequence length: 489

Sequence type: Nucleic acid

Strandedness: Double

WO 98/21328

123

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Fibrosarcoma

Cell line: HT-1080

Clone name: HP10050

Sequence description

ATGGCGGCTG	GGCTGTTTGG	TTTGAGCGCT	CGCCGTCTTT	TGGCGGCAGC	GGCGACGCGA	60
GGGCTCCCCG	CCGCCCCGCT	CCGCTGGGAA	TCTAGCTTCT	CCAGGACTGT	GGTCGCCCCG	120
TCCGCTGTGG	CGGGAAAGCG	GCCCCCAGAA	CCGACCACAC	CGTGGCAAGA	GGACCCAGAA	180
CCCAGGACG	AAAAC TTGTA	TGAGAAGAAC	CCAGACTCCC	ATGGTTATGA	CAAGGACCCC	240
GTTTTGGACG	TCTGGAACAT	GCGACTTGTC	TTCTTCTTTG	GCGTCTCCAT	CATCCTGGTC	300
CTTGGCAGCA	CCTTTGTGGC	CTATCTGCCT	GACTACAGGT	GCACAGGGTG	TCCAAGAGCG	360
TGGGATGGGA	TGAAAGAGTG	GTCCCCCGCG	GAAGCTGAGA	GGCTTGTGAA	ATACCGAGAG	420
GCCAATGGCC	TTCCCATCAT	GGAATCCAAC	TGCTTCGACC	CCAGCAAGAT	CCAGCTGCCA	480
GAGGATGAG						489

Sequence No.: 34

Sequence length: 276

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Stomach cancer

Clone name: HP10071

Sequence description

ATGACGAAAT	TAGCGCAGTG	GCTTTGGGGA	CTAGCGATCC	TGGGCTCCAC	CTGGGTGGCC	60
CTGACCACGG	GAGCCTTGGG	CCTGGAGCTG	CCCTTGTCCT	GCCAGGAAGT	CCTGTGGCCA	120
CTGCCCCCCT	ACTTGCTGGT	GTCCGCCCGC	TGCTATGCCC	TGGGCACTGT	GGGCTATCGT	180
GTGGCCACTT	TTCATGACTG	CGAGGACGCC	GCACGCGAGC	TGCAGAGCCA	GATACAGGAG	240
GCCCCGAGCCG	ACTTAGCCCCG	CAGGGGGCTG	CGCTTC			276

Sequence No.: 35

Sequence length: 516

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

124

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Lymphoma

Cell line: U937

Clone name: HP10076

Sequence description

ATGGAATATT	TGGCTCATCC	CAGTACACTC	GGCTTGGCTG	TTGGAGTTGC	TTGTGGCATG	60
TGCCTGGGCT	GGAGCCTTCG	AGTATGCTTT	GGGATGCTCC	CCAAAAGCAA	GACGAGCAAG	120
ACACACACAG	ATACTGAAAG	TGAAGCAAGC	ATCTTGGGAG	ACACCGGGGA	GTACAAGATG	180
ATTCTTGTGG	TTCGAAATGA	CTTAAAGATG	GGAAAAGGGA	AAGTGGCTGC	CCAGTGCTCT	240
CATGCTGCTG	TTTCAGCCTA	CAAGCAGATT	CAAAGAAGAA	ATCCTGAAAT	GCTCAAACAA	300
TGGGAATACT	GTGGCCAGCC	CAAGGTGGTG	GTCAAAGCTC	CTGATGAAGA	AACCCTGATT	360
GCATTATTGG	CCCATGCAAA	AATGCTGGGA	CTGACTGTAA	GTTTAATTCA	AGATGCTGGA	420
CGTACTCAGA	TTGCACCAGG	CTCTCAAAC	GTCTAGGGA	TTGGGCCAGG	ACCAGCAGAC	480
CTAATTGACA	AAGTCACTGG	TCACCTAAAA	CTTTAC			516

Sequence No.: 36

Sequence length: 447

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Lymphoma

Cell line: U937

Clone name: HP10085

Sequence description

ATGATGACCA	AACATAAAAA	GTGTTTTATA	ATTGTTGGTG	TTTAAATAAC	AACTAATATT	60
ATTACTCTGA	TAGTTAAACT	AACTCGAGAT	TCTCAGAGTT	TATGCCCTTA	TGATTGGATT	120
GGTTTCCAAA	ACAAATGCTA	TTATTTCTCT	AAAGAAGAAG	GAGATTGGAA	TTCAAGTAAA	180
TACAACTGTT	CCACTCAACA	TGCCGACCTA	ACTATAATTG	ACAACATAGA	AGAAATGAAT	240
TTTCTTAGGC	GGTATAAATG	CAGTTCTGAT	CACTGGATTG	GACTGAAGAT	GGCAAAAAAT	300
CGAACAGGAC	AATGGGTAGA	TGGAGCTACA	TTTACCAAAT	CGTTTGGCAT	GAGAGGGAGT	360
GAAGGATGTG	CCTACCTCAG	CGATGATGGT	GCAGCAACAG	CTAGATGTTA	CACCGAAAGA	420
AAATGGATTT	GCAGGAAAAG	AATACAC				447

Sequence No.: 37

Sequence length: 564

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Stomach cancer

Clone name: HP10122

Sequence description

ATGAGCACTA	TGTTGCGGGA	CACTCTCCTC	ATCGTTTTTA	TCTCTGTGTG	CACGGCTCTG	60
CTGCGAGAGG	GCATAACCTG	GGTCCTGGTT	TACAGGACAG	ACAAGTACAA	GAGACTGAAG	120
GCAGAAGTGG	AAAAACAGAG	TAAAAAATTG	GAAAAGAAGA	AGGAAACAAT	AACAGAGTCA	180
GCTGGTCGAC	AACAGAAAAA	GAAAATAGAG	AGACAAGAAG	AGAAACTGAA	GAATAACAAC	240
AGAGATCTAT	CAATGGTTTCG	AATGAAATCC	ATGTTTGCTA	TTGGCTTTTG	TTTTACTGCC	300
CTAATGGGAA	TGTTCAATTC	CATATTTGAT	GGTAGAGTGG	TGGCAAAGCT	TCCTTTTACC	360
CCTCTTTCTT	ACATCCAAGG	ACTGTCTCAT	CGAAATCTGC	TGGGAGATGA	CACCACAGAC	420
TGTTCCTTCA	TTTTCTGTGA	TATTCTCTGT	ACTATGTCTG	TTCGACAGAA	CATTTCAGAAG	480
ATTCTCGGCC	TTGCCCCTTC	ACGAGCCGCC	ACCAAGCAGG	CAGGTGGATT	TCTTGGCCCA	540
CCACCTCCTT	CTGGGAAGTT	CTCT				564

Sequence No.: 38

Sequence length: 645

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Lymphoma

Cell line: U937

Clone name: HP10136

Sequence description

ATGGTGTTC	TAACAATGAT	CGCCCGAGTG	GCGGACGGGC	TCCCGCTGGC	CGCCTCGATG	60
CAGGAGGACG	AACAGTCTGG	CCGGGACCTT	CAACAGTATC	AGAGTCAGGC	TAAGCAACTC	120
TTTCGAAAGT	TGAATGAACA	GTCCCCTACC	AGATGTACCT	TGGAAGCAGG	AGCCATGACT	180
TTTCACTACA	TTATTGAGCA	GGGGGTGTGT	TATTTGGTTT	TATGTGAAGC	TGCCTTCCCT	240
AAGAAGTTGG	CTTTTGCTTA	CCTAGAAGAT	TTGCACTCAG	AATTTGATGA	ACAGCATGGA	300
AAGAAGGTGC	CCACTGTGTC	CCGACCCTAT	TCCTTTATTG	AATTTGATAC	TTTCATTGAG	360
AAAACCAAGA	AGCTCTACAT	TGACAGTCGT	GCTCGAAGAA	ATCTAGGCTC	CATCAACACT	420
GAATTGCAAG	ATGTGCAGAG	GATCATGGTG	GCCAATATTG	AAGAAGTGTT	ACAACGAGGA	480
GAAGCACTCT	CAGCATTGGA	TTCAAAGGCT	AACAATTTGT	CCAGTCTGTC	CAAGAAATAC	540

126

CGCCAGGATG CGAAGTACTT GAACATGCGT TCCACTTATG CCAAAGTTGC AGCAGTAGCT 600
GTATTTTCA TCATGTTAAT AGTGTATGTC CGATTCTGGT GGCTG 645

Sequence No.: 39
Sequence length: 336
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
Organism species: *Homo sapiens*
Cell kind: Stomach cancer
Clone name: HP10175

Sequence description

ATGCAGGACA CTGGCTCAGT AGTGCCTTTG CATTGGTTTG GCTTTGGCTA CGCAGCACTG 60
GTTGCTTCTG GTGGGATCAT TGGCTATGTA AAAGCAGGCA GCGTGCCGTC CCTGGCTGCA 120
GGGCTGCTCT TTGGCAGTCT AGCCGGCCTG GGTGCTTACC AGCTGTCTCA GGATCCAAGG 180
AACGTTTGGG TTTTCCTAGC TACATCTGGT ACCTTGGCTG GCATTATGGG AATGAGGTTT 240
TACCACTCTG GAAAATTCAT GCCTGCAGGT TTAATTGCAG GTGCCAGTTT GCTGATGGTC 300
GCCAAAGTTG GAGTTAGTAT GTCAACAGA CCCCAT 336

Sequence No.: 40
Sequence length: 342
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
Organism species: *Homo sapiens*
Cell kind: Epidermoid carcinoma
Cell line: KB
Clone name: HP10179

Sequence description

ATGGAGAAGC CCCTCTTCCC ATTAGTGCCCT TTGCATTGGT TTGGCTTTGG CTACACAGCA 60
CTGGTTGTTT CTGGTGGGAT CGTTGGCTAT GTAAAAACAG GCAGCGTGCC GTCCCTGGCT 120
GCAGGGCTGC TCTTCGGCAG TCTAGCCGGC CTGGGTGCTT ACCAGCTGTA TCAGGATCCA 180
AGGAACGTTT GGGGTTTCCT AGCCGCTACA TCTGTACTT TTGTTGGTGT TATGGGAATG 240
AGATCCTACT ACTATGGAAA ATTCATGCCT GTAGGTTTAA TTGCAGGTGC CAGTTTGCTG 300
ATGGCCGCCA AAGTTGGAGT TCGTATGTTG ATGACATCTG AT 342

Sequence No.: 41
Sequence length: 981
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
Organism species: *Homo sapiens*
Cell kind: Fibrosarcoma
Cell line: HT-1080
Clone name: HP10196
Sequence description

ATGGCGGCGG CGGCGGCGGC GGCTGCAGCT ACGAACGGGA CCGGAGGAAG CAGCGGGATG	60
GAGGTGGATG CAGCAGTAGT CCCCAGCGTG ATGGCCTGCG GAGTGA CTGG GAGTGTTTCC	120
GTCGCTCTCC ATCCCCTTGT CATTCTCAAC ATCTCAGACC ACTGGATCCG CATGCGCTCC	180
CAGGAGGGGC GGCCTGTGCA GGTGATTGGG GCTCTGATTG GCAAGCAGGA GGGCCGAAAT	240
ATCGAGGTGA TGAATCCTT TGAGCTGCTG TCCACACCG TGAAGAGAA GATTATCATT	300
GACAAGGAAT ATTATTACAC CAAGGAGGAG CAGTTTAAAC AGGTGTTCAA GGAGCTGGAG	360
TTTCTGGGTT GGTATACCAC AGGGGGGCCA CCTGACCCCT CGGACATCCA CGTCCATAAG	420
CAGGTGTGTG AGATCATCGA GAGCCCCCTC TTTCTGAAGT TGAACCCTAT GACCAAGCAC	480
ACAGATCTTC CTGTACCGT TTTTGAGTCT GTCATTGATA TAATCAATGG AGAGGCCACA	540
ATGCTGTTTG CTGAGCTGAC CTACACTCTG GCCACAGAGG AAGCGGAACG CATTGGTGTA	600
GACCACGTAG CCCGAATGAC AGCAACAGGC AGTGGAGAGA ACTCCACTGT GGCTGAACAC	660
CTGATAGCAC AGCACAGCGC CATCAAGATG CTGCACAGCC GCGTCAAGCT CATCTTGGAG	720
TACGTCAAGG CCTCTGAAGC GGGAGAGGTC CCCTTTAATC ATGAGATCCT GCGGGAGGCC	780
TATGCTCTGT GTCAGTGTCT CCCGGTGCTC AGCACAGACA AGTTCAAGAC AGATTTTAT	840
GATCAATGCA ACGACGTGGG GCTCATGGCC TACCTCGGCA CCATCACCAA AACGTGCAAC	900
ACCATGAACC AGTTTGTGAA CAAGTTCAAT GTCCTCTACG ACCGACAAGG CATCGGCAGG	960
AGAATGCGCG GGCTCTTTTT C	981

Sequence No.: 42
Sequence length: 1119
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
Organism species: *Homo sapiens*
Cell kind: Fibrosarcoma
Cell line: HT-1080
Clone name: HP10235
Sequence description

ATGACCTAT	GTGCCATGCT	CCCCCTGCTG	TTATTCACCT	ACCTCAACTC	CTTCCTGCAT	60
CAGAGGATCC	CCCAGTCCGT	ACGGATCCTG	GGCAGCCTGG	TGGCCATCCT	GCTGGTGTTT	120
CTGATCACTG	CCATCCTGGT	GAAGGTGCAG	CTGGATGCTC	TGCCCTTCTT	TGTCATCACC	180
ATGATCAAGA	TCGTGCTCAT	TAATTCATTT	GGTGCCATCC	TGCAGGGCAG	CCTGTTTGGT	240
CTGGCTGGCC	TTCTGCCTGC	CAGCTACACG	CCCCCATCA	TGAGTGCCCA	GGGCCTAGCA	300
GGCTTCTTTG	CCTCCGTGGC	CATGATCTGC	GCTATTGCCA	GTGGCTCGGA	GCTATCAGAA	360
AGTGCCTTCG	GCTACTTTAT	CACAGCCTGT	GCTGTTATCA	TTTTGACCAT	CATCTGTTAC	420
CTGGGCCTGC	CCCGCCTGGA	ATTCTACCGC	TACTACCAGC	AGCTCAAGCT	TGAAGGACCC	480
GGGGAGCAGG	AGACCAAGTT	GGACCTCATT	AGCAAAGGAG	AGGAGCCAAG	AGCAGGCAAA	540
GAGGAATCTG	GAGTTTCAGT	CTCCAACCTCT	CAGCCCACCA	ATGAAAGCCA	CTCTATCAAA	600
GCCATCCTGA	AAAATATCTC	AGTCCTGGCT	TTCTCTGTCT	GCTTCATCTT	CACTATCACC	660
ATTGGGATGT	TTCCAGCCGT	GACTGTTGAG	GTCAAGTCCA	GCATCGCAGG	CAGCAGCACC	720
TGGGAACGTT	ACTTCATTCC	TGTGTCCTGT	TTCTTGACTT	TCAATATCTT	TGACTGGTTG	780
GGCCGGAGCC	TCACAGCTGT	ATTGATGTGG	CCTGGGAAGG	ACAGCCGCTG	GCTGCCAAGC	840
CTGGTGCTGG	CCCGGCTGGT	GTTTGTGCCA	CTGCTGCTGC	TGTGCAACAT	TAAGCCCCGC	900
CGCTACCTGA	CTGTGGTCTT	CGAGCACGAT	GCCTGGTTCA	TCTTCTTCAT	GGCTGCCTTT	960
GCCTTCTCCA	ACGGCTACCT	CGCCAGCCTC	TGCATGTGCT	TCGGGCCCCA	GAAAGTGAAG	1020
CCAGCTGAGG	CAGAGACCGC	AGGAGCCATC	ATGGCCTTCT	TCCTGTGTCT	GGGTCTGGCA	1080
CTGGGGGCTG	TTTTCTCCTT	CCTGTTCCGG	GCAATTGTG			1119

Sequence No.: 43

Sequence length: 549

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Stomach cancer

Clone name: HP10297

Sequence description

ATGAAGCTCT	TATCTTTGGT	GGCTGTGGTC	GGGTGTTTGC	TGGTGCCCCC	AGCTGAAGCC	60
AACAAGAGTT	CTGAAGATAT	CCGGTGCAAA	TGCATCTGTC	CACCTTATAG	AAACATCAGT	120
GGGCACATTT	ACAACCAGAA	TGTATCCCAG	AAGGACTGCA	ACTGCCTGCA	CGTGGTGGAG	180
CCCATGCCAG	TGCCTGGCCA	TGACGTGGAG	GCCTACTGCC	TGCTGTGCGA	GTGCAGGTAC	240
GAGGAGCGCA	GCACCACCAC	CATCAAGGTC	ATCATTGTCA	TCTACCTGTC	CGTGGTGGGT	300
GCCCTGTTGC	TCTACATGGC	CTTCCTGATG	CTGGTGGACC	CTCTGATCCG	AAAGCCGGAT	360
GCATACACTG	AGCAACTGCA	CAATGAGGAG	GAGAATGAGG	ATGCTCGCTC	TATGGCAGCA	420
GCTGCTGCAT	CCCTCGGGGG	ACCCCGAGCA	AACACAGTCC	TGGAGCGTGT	GGAAGGTGCC	480
CAGCAGCGGT	GGAAGCTGCA	GGTGCAGGAG	CAGCGGAAGA	CAGTCTTCGA	TCGGCACAAG	540
ATGCTCAGC						549

Sequence No.: 44

Sequence length: 348

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Stomach cancer

Clone name: HP10299

Sequence description

ATGGCCAGTA	CAGTGGTAGC	AGTTGGACTG	ACCATTGCTG	CTGCAGGATT	TGCAGGCCGT	60
TACGTTTTGC	AAGCCATGAA	GCATATGGAG	CCTCAAGTAA	AACAAGTTTT	TCAAAGCCTA	120
CCAAAATCTG	CCTTCAGTGG	TGGCTATTAT	AGAGGTGGGT	TTGAACCCAA	AATGACAAAA	180
CGGGAAGCA	GCATTAATAC	TAGGTGTAAG	CCCTACTGCC	AATAAAGGGA	AAATAAGAGA	240
GCTCATCGAC	GAATTATGCT	TTTAAATCAT	CCTGACAAAG	GAGGATCTCC	TTATATAGCA	300
GCCAAAATCA	ATGAAGCTAA	AGATTTACTA	GAAGGTCAAG	CTAAAAAA		348

Sequence No.: 45

Sequence length: 456

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Epidermoid carcinoma

Cell line: KB

Clone name: HP10301

Sequence description

ATGGCTGTCC	TCTCTAAGGA	ATATGGTTTT	GTGCTTCTAA	CTGGTGCTGC	CAGCTTTATA	60
ATGGTGGCCC	ACCTAGCCAT	CAATGTTTCC	AAGGCCCGCA	AGAAGTACAA	AGTGGAGTAT	120
CCTATCATGT	ACAGCACGGA	CCCTGAAAAT	GGGCACATCT	TCAACTGCAT	TCAGCGAGCC	180
CACCAGAACA	CGTTGGAAGT	GTATCCTCCC	TTCTTATTTT	TTCTAGCTGT	TGGAGGTGTT	240
TACCACCCGC	GTATAGCTTC	TGGCCTGGGC	TTGGCCTGGA	TTGTTGGACG	AGTTCTTTAT	300
GCTTATGGCT	ATTACACGGG	AGAACCCAGC	AAGCGTAGTC	GAGGAGCCCT	GGGGTCCATC	360
GCCCTCCTGG	GCTTGGTGGG	CACAACTGTG	TGCTCTGCTT	TCCAGCATCT	TGGTTGGGTT	420
AAAAGTGGCT	TGGGCAGTGG	ACCCAAATGC	TGCCAT			456

Sequence No.: 46
Sequence length: 1677
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
Organism species: *Homo sapiens*
Cell kind: Liver
Clone name: HP10302
Sequence description

ATGGCCCCCA	CGCTGCAACA	GGCGTACCGG	AGGCGCTGGT	GGATGGCCTG	CACGGCTGTG	60
CTGGAGAACC	TCTTCTTCTC	TGCTGTACTC	CTGGGCTGGG	GCTCCCTGTT	GATCATTCTG	120
AAGAACGAGG	GCTTCTATTG	CAGCACGTGC	CCAGCTGAGA	GCAGCACCAA	CACCACCCAG	180
GATGAGCAGC	GCAGGTGGCC	AGGCTGTGAC	CAGCAGGACG	AGATGCTCAA	CCTGGGCTTC	240
ACCATTGGTT	CCTTCGTGCT	CAGCGCCACC	ACCCTGCCAC	TGGGGATCCT	CATGGACCGC	300
TTTGGCCCCC	GACCCGTGCG	GCTGGTTGGC	AGTGCCTGCT	TCACTGCGTC	CTGCACCCCTC	360
ATGGCCCTGG	CCTCCCGGGA	CGTGGAAGCT	CTGTCTCCGT	TGATATTCCT	GGCGCTGTCC	420
CTGAATGGCT	TTGGTGGCAT	CTGCCTAAGC	TTCACCTTAC	TCACGCTGCC	CAACATGTTT	480
GGGAACCTGC	GCTCCACGTT	AATGGCCCTC	ATGATTGGCT	CTTACGCCTC	TTCTGCCATT	540
ACGTTCCAG	GAATCAAGCT	GATCTACGAT	GCCGGTGTGG	CCTTCGTGGT	CATCATGTTC	600
ACCTGGTCTG	GCCTGGCCTG	CCTTATCTTT	CTGAACTGCA	CCCTCAACTG	GCCCATCGAA	660
GCCTTTCTG	CCCCTGAGGA	AGTCAATTAC	ACGAAGAAGA	TCAAGCTGAG	TGGGCTGGCC	720
CTGGACCACA	AGGTGACAGG	TGACCTCTTC	TACACCCATG	TGACCACCAT	GGGCCAGAGG	780
CTCAGCCAGA	AGGCCCCAG	CCTGGAGGAC	GGTTCGGATG	CCTTCATGTC	ACCCCAGGAT	840
GTTGCGGGCA	CCTCAGAAAA	CCTTCCTGAG	AGGTCTGTCC	CCTTACGCAA	GAGCCTCTGC	900
TCCCCCACTT	TCCTGTGGAG	CCTCCTCACC	ATGGGCATGA	CCCAGCTGCG	GATCATCTTC	960
TACATGGCTG	CTGTGAACAA	GATGCTGGAG	TACCTTGTGA	CTGGTGGCCA	GGAGCATGAG	1020
ACAAATGAAC	AGCAACAAAA	GGTGGCAGAG	ACAGTTGGGT	TCTACTCCTC	CGTCTTCGGG	1080
GCCATGCAGC	TGTTGTGCCT	TCTCACCTGC	CCCCTCATTG	GCTACATCAT	GGACTGGCGG	1140
ATCAAGGACT	GCGTGGACGC	CCCAACTCAG	GGCACTGTCC	TCGGAGATGC	CAGGGACGGG	1200
GTTGCTACCA	AATCCATCAG	ACCACGCTAC	TGCAAGATCC	AAAAGCTCAC	CAATGCCATC	1260
AGTGCCTTCA	CCCTGACCAA	CCTGCTGCTT	GTGGGTTTTG	GCATCACCTG	TCTCATCAAC	1320
AACTTACACC	TCCAGTTTGT	GACCTTTGTC	CTGCACACCA	TTGTTGAGG	TTTCTTCCAC	1380
TCAGCCTGTG	GGAGTCTCTA	TGCTGCAGTG	TTCCCATCCA	ACCACTTTGG	GACGCTGACA	1440
GGCCTGCAGT	CCCTCATCAG	TGCTGTGTTT	GCCTTGCTTC	AGCAGCCACT	TTTCATGGCG	1500
ATGGTGGGAC	CCCTGAAAGG	AGAGCCCTTC	TGGGTGAATC	TGGGCCTCCT	GCTATTCTCA	1560
CTCCTGGGAT	TCCTGTTGCC	TTCTTACCTC	TTCTATTACC	GTGCCC GGCT	CCAGCAGGAG	1620
TACGCCGCCA	ATGGGATGGG	CCCACTGAAG	GTGCTTAGCG	GCTCTGAGGT	GACCGCA	1677

Sequence No.: 47
Sequence length: 990

WO 98/21328

131

Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
Organism species: *Homo sapiens*
Cell kind: Osteosarcoma
Cell line: U-2 OS
Clone name: HP10304
Sequence description

ATGGAGGGCG CTCACCGGG GTCGCTCGCC CTCGGGCTCC TGCTGTTCTG GCGCTACCC 60
GCCTCCGGCT GGCTGACGAC GGGCGCCCC GAGCCGCCG CGCTGTCCGG AGCCCCACAG 120
GACGGCATCA GAATTAATGT AACTACACTG AAAGATGATG GGGACATATC TAAACAGCAG 180
GTTGTTCTTA ACATAACCTA TGAGAGTGGA CAGGTGTATG TAAATGACTT ACCTGTAAAT 240
AGTGGTGTA CCCGAATAAG CTGTCAGACT TTGATAGTGA AGAATGAAAA TCTTGAAAAAT 300
TTGGAGGAAA AAGAATATTT TGAATTGTC AGTGTAAGGA TTTTAGTTCA TGAGTGGCCT 360
ATGACATCTG GTTCCAGTTT GCAACTAATT GTCATTCAAG AAGAGGTAGT AGAGATTGAT 420
GGAAAAAAG TTCAGCAAAA GGATGTCACT GAAATTGATA TTTTAGTTAA GAACCGGGGA 480
GTACTCAGAC ATTCAAATA TACCCTCCCT TTGGAAGAAA GCATGCTCTA CTCTATTTCT 540
CGAGACAGTG ACATTTTATT TACCCTTCCT AACCTCTCCA AAAAAGAAA TGTTAGTTCA 600
CTGCAAAACCA CTAGCCAGTA TCTTATCAGG AATGTGGAAG CCACTGTAGA TGAAGATGTT 660
TTACCTGGCA AGTTACCTGA AACTCCTCTC AGAGCAGAGC CGCCATCTTC ATATAAGGTA 720
ATGTGTCAGT GGATGGAAAA GTTTAGAAAA GATCTGTGTA GGTTCCTGGAG CAACGTTTTC 780
CCAGTATTCT TTCAGTTTTT GAACATCATG GTGGTTGGAA TTACAGGAGC AGCTGTGGTA 840
ATAACCATCT TAAAGGTGTT TTTCCAGTT TCTGAATACA AAGGAATTCT TCAGTTGGAT 900
AAAGTGGACG TCATACCTGT GACAGCTATC AACTTATATC CAGATGGTCC AGAGAAAAGA 960
GCTGAAAACC TTGAAGATAA AACATGTATT 990

Sequence No.: 48
Sequence length: 324
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
Organism species: *Homo sapiens*
Cell kind: Osteosarcoma
Cell line: U-2 OS
Clone name: HP10305
Sequence description

ATGAGTCTGA CTTCCAGTTC CAGCGTACGA GTTGAATGGA TCGCAGCAGT TACCATTGCT 60

132

GCTGGGACAG CTGCAATTGG TTATCTAGCT TACAAAAGAT TTTATGTTAA AGATCATCGA 120
AATAAAGCTA TGATAAACCT TCACATCCAG AAAGACAACC CCAAGATAGT ACATGCTTTT 180
GACATGGAGG ATTTGGGAGA TAAAGCTGTG TACTGCCGTT GTTGGAGGTC CAAAAAGTTC 240
CCATTCTGTG ATGGGGCTCA CACAAAACAT AACGAAGAGA CTGGAGACAA TGTGGGCCCT 300
CTGATCATCA AGAAAAAAGA AACT 324

Sequence No.: 49

Sequence length: 303

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Oosterosarcoma

Cell line: U-2 OS

Clone name: HP10306

Sequence description

ATGAACCTGG AGCGAGTGTG CAATGAGGAG AAATTGAACC TGTGCCGGAA GTACTACCTG 60
GGGGGGTTTG CTTTCCTGCC TTTTCTCTGG TTGGTCAACA TCTTCTGGTT CTTCCGAGAG 120
GCCTTCCTTG TCCAGCCTA CACAGAACAG AGCCAAATCA AAGGCTATGT CTGGCGCTCA 180
GCTGTGGGCT TCCTCTTCTG GGTGATAGTG CTCACCTCCT GGATCACCAT CTTCCAGATC 240
TACCGGCCCC GCTGGGGTGC CCTTGGGGAC TACCTCTCCT TCACCATACC CCTGGGCACC 300
CCC 303

Sequence No.: 50

Sequence length: 1116

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Epidermoid carcinoma

Cell line: KB

Clone name: HP10328

Sequence description

ATGAAGTATC TCCGGCACCG GCGGCCCAAT GCCACCCTCA TTCTGGCCAT CGGCGCTTTC 60
ACCCTCCTCC TCTTCAGTCT GCTAGTGTCA CCACCCACCT GCAAGGTCCA GGAGCAGCCA 120
CCGGCGATCC CCGAGGCCCT GGCCTGGCCC ACTCCACCCA CCCGCCCAGC CCCGGCCCCG 180

```

TGCCATGCCA ACACCTCTAT GGTCACCCAC CCGGACTTCG CCACGCAGCC GCAGCACGTT 240
CAGAACTTCC TCCTGTACAG AACTGCCCC CACTTTCCCC TGCTGCAGGA CGTGCCCCCC 300
TCTAAGTCCG CGCAGCCGGT CTTCCCTGCTG CTGGTGATCA AGTCCTCCCC TAGCAACTAT 360
GTGCGCCGCG AGCTGCTGCG GCGCACGTGG GGCCGCGAGC GCAAGGTACG GGGTTTGCAG 420
CTGCGCCTCC TCTTCTGGT GGGCACAGCC TCCAACCCGC ACGAGGCCCG CAAGGTCAAC 480
CGGCTGCTGG AGCTGGAGGC ACAGACTCAC GGAGACATCC TGCAGTGGGA CTTCCACGAC 540
TCCTTCTTCA ACCTCACGCT CAAGCAGGTC CTGTTCTTAC AGTGGCAGGA GACAAGGTGC 600
GCCAACGCCA GCTTCGTGCT CAACGGGGAT GATGACGTCT TTGCACACAC AGACAACATG 660
GTCTTCTACC TGCAGGACCA TGACCCTGGC CGCCACCTCT TCGTGGGGCA ACTGATCCAA 720
AACGTGGGCC CCATCCGGGC TTTTGGAGC AAGTACTATG TGCCAGAGGT GGTGACTCAG 780
AATGAGCGGT ACCCACCCTA TTGTGGGGGT GGTGGCTTCT TGCTGTCCCG CTTACGGGCC 840
GCTGCCCTGC GCGTGCTGC CCATGTCTTG GACATCTTCC CCATTGATGA TGTCTTCCTG 900
GGTATGTGTC TGGAGCTTGA GGGACTGAAG CCTGCCTCCC ACAGCGGCAT CCGCACGTCT 960
GGCGTGCGGG CTCCATCGCA ACACCTGTCC TCCTTTGACC CCTGCTTCTA CCGAGACCTG 1020
CTGCTGGTGC ACCGCTTCCT ACCTTATGAG ATGCTGCTCA TGTGGGATGC GCTGAACCAG 1080
CCCAACCTCA CCTGCGGCAA TCAGACACAG ATCTAC 1116

```

Sequence No.: 51

Sequence length: 986

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Fibrosarcoma

Cell line: HT-1080

Clone name: HP00442

Sequence characteristics

Code representing characteristics: CDS

Existence site: 82.. 699

Characterization method: E

Sequence description

```

AGACTGCGGG ACGGACGGTG GACGCTGGGA CGCGTTTGTA GCTCCGGCCC CGCCGTTCCG 60
ACCCCCGCCG CCGTCGCCGC C ATG ACG GGG CTA GCA CTG CTC TAC TCC GGG 111
Met Thr Gly Leu Ala Leu Leu Tyr Ser Gly
1 5 10
GTC TTC GTG GCC TTC TGG GCC TGC GCG CTG GCC GTG GGA GTC TGC TAC 159
Val Phe Val Ala Phe Trp Ala Cys Ala Leu Ala Val Gly Val Cys Tyr
15 20 25
ACC ATT TTT GAT TTG GGC TTC CGC TTT GAT GTG GCA TGG TTC CTG ACG 207
Thr Ile Phe Asp Leu Gly Phe Arg Phe Asp Val Ala Trp Phe Leu Thr

```

134

30	35	40	
GAG ACT TCG CCC TTC ATG TGG TCC AAC CTG GGC ATT GGC CTA GCT ATC			255
Glu Thr Ser Pro Phe Met Trp Ser Asn Leu Gly Ile Gly Leu Ala Ile			
45	50	55	
TCC CTG TCT GTG GTT GGG GCA GCC TGG GGC ATC TAT ATT ACC GGC TCC			303
Ser Leu Ser Val Val Gly Ala Ala Trp Gly Ile Tyr Ile Thr Gly Ser			
60	65	70	
TCC ATC ATT GGT GGA GGA GTG AAG GCC CCC AGG ATC AAG ACC AAG AAC			351
Ser Ile Ile Gly Gly Gly Val Lys Ala Pro Arg Ile Lys Thr Lys Asn			
75	80	85	90
CTG GTC AGC ATC ATC TTC TGT GAG GCT GTG GCC ATC TAC GGC ATC ATC			399
Leu Val Ser Ile Ile Phe Cys Glu Ala Val Ala Ile Tyr Gly Ile Ile			
95	100	105	
ATG GCA ATT GTC ATT AGC AAC ATG GCT GAG CCT TTC AGT GCC ACA GAC			447
Met Ala Ile Val Ile Ser Asn Met Ala Glu Pro Phe Ser Ala Thr Asp			
110	115	120	
CCC AAG GCC ATC GGC CAT CGG AAC TAC CAT GCA GGC TAC TCC ATG TTT			495
Pro Lys Ala Ile Gly His Arg Asn Tyr His Ala Gly Tyr Ser Met Phe			
125	130	135	
GGG GCT GGC CTC ACC GTA GGC CTG TCT AAC CTC TTC TGT GGA GTC TGC			543
Gly Ala Gly Leu Thr Val Gly Leu Ser Asn Leu Phe Cys Gly Val Cys			
140	145	150	
GTG GGC ATC GTG GGC AGT GGG GCT GCC CTG GCC GAT GCT CAG AAC CCC			591
Val Gly Ile Val Gly Ser Gly Ala Ala Leu Ala Asp Ala Gln Asn Pro			
155	160	165	170
AGC CTC TTT GTA AAG ATT CTC ATC GTG GAG ATC TTT GGC AGC GCC ATT			639
Ser Leu Phe Val Lys Ile Leu Ile Val Glu Ile Phe Gly Ser Ala Ile			
175	180	185	
GGC CTC TTT GGG GTC ATC GTC GCA ATT CTT CAG ACC TCC AGA GTG AAG			687
Gly Leu Phe Gly Val Ile Val Ala Ile Leu Gln Thr Ser Arg Val Lys			
190	195	200	
ATG GGT GAC TAGATGATAT GTGTGGGTGG GGCCGTGCCT CACT			730
Met Gly Asp			
205			
TTTATTTTATT GCTGGTTTTTC CTGGGACAGC TGGAGCTGTG TCCCTTAGCC TTTCAGAGGC			790
TTGGTGTTCA GGGCCCTCCC TGCACTCCCC TCTTGCTGCG TGTTGATTTC GAGGCACTGC			850
AGTCCAGGCC GAGTCCTCAG TCGGGGAGC AGGCTGCTGC TGCTGACTCT GTGCAGCTGC			910
GCACCTGTGT CCCCCACCTC CACCCTCAAC CCATCTTCCT AGTGTTTGTG AAATAAACTT			970
GGTATTTGTC TGGGTC			986

Sequence No.: 52

Sequence length: 1824

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Leukocyte

Clone name: HP00804

Sequence characteristics

Code representing characteristics: CDS

Existence site: 133.. 1248

Characterization method: E

Sequence description

```

GGCCCAGCTG AGCGGCCGCC GAGCGGGTGC GGGTGCGGGC GCATCGGCCA TCACCGCGCG      60
GCCGCGCAGC GGACACCGTG CGTACCGGCC TCGGCGCGCC GGCCACCGGG GCGGACCGCG      120
GAACCCGAGG CC ATG TCC CAT GAA AAG AGT TTT TTG GTG TCT GGG GAC AAC      171
      Met Ser His Glu Lys Ser Phe Leu Val Ser Gly Asp Asn
              1              5              10
TAT CCT CCC CCC AAC CCT GGA TAT CCG GGG GGG CCC CAG CCA CCC ATG      219
Tyr Pro Pro Pro Asn Pro Gly Tyr Pro Gly Gly Pro Gln Pro Pro Met
      15              20              25
CCC CCC TAT GCT CAG CCT CCC TAC CCT GGG GCC CCT TAC CCA CAG CCC      267
Pro Pro Tyr Ala Gln Pro Pro Tyr Pro Gly Ala Pro Tyr Pro Gln Pro
      30              35              40              45
CCT TTC CAG CCC TCC CCC TAC GGT CAG CCA GGG TAC CCC CAT GGC CCC      315
Pro Phe Gln Pro Ser Pro Tyr Gly Gln Pro Gly Tyr Pro His Gly Pro
              50              55              60
AGC CCC TAC CCC CAA GGG GGC TAC CCA CAG GGT CCC TAC CCC CAA GGG      363
Ser Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Gly
      65              70              75
GGC TAC CCA CAG GGC CCC TAC CCA CAA GAG GGC TAC CCA CAG GGC CCC      411
Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Glu Gly Tyr Pro Gln Gly Pro
      80              85              90
TAC CCC CAA GGG GGC TAC CCC CAG GGG CCA TAT CCC CAG AGC CCC TTC      459
Tyr Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Ser Pro Phe
      95              100              105
CCC CCC AAC CCC TAT GGA CAG CCA CAG GTC TTC CCA GGA CAA GAC CCT      507
Pro Pro Asn Pro Tyr Gly Gln Pro Gln Val Phe Pro Gly Gln Asp Pro
      110              115              120              125
GAC TCA CCC CAG CAT GGA AAC TAC CAG GAG GAG GGT CCC CCA TCC TAC      555
Asp Ser Pro Gln His Gly Asn Tyr Gln Glu Glu Gly Pro Pro Ser Tyr
              130              135              140
TAT GAC AAC CAG GAC TTC CCT GCC ACC AAC TGG GAT GAC AAG AGC ATC      603
Tyr Asp Asn Gln Asp Phe Pro Ala Thr Asn Trp Asp Asp Lys Ser Ile

```

136

145	150	155	651
CGA CAG GCC TTC ATC CGC AAG GTG	TTC CTA GTG CTG ACC TTG CAG CTG		
Arg Gln Ala Phe Ile Arg Lys Val	Phe Leu Val Leu Thr Leu Gln Leu		
160	165	170	699
TCG GTG ACC CTG TCC ACG GTG TCT	GTG TTC ACT TTT GTT GCG GAG GTG		
Ser Val Thr Leu Ser Thr Val Ser	Val Phe Thr Phe Val Ala Glu Val		
175	180	185	747
AAG GGC TTT GTC CGG GAG AAT GTC	TGG ACC TAC TAT GTC TCC TAT GCT		
Lys Gly Phe Val Arg Glu Asn Val	Trp Thr Tyr Tyr Val Ser Tyr Ala		
190	195	200	795
GTC TTC TTC ATC TCT CTC ATC GTC	CTC AGC TGT TGT GGG GAC TTC CGG		
Val Phe Phe Ile Ser Leu Ile Val	Leu Ser Cys Cys Gly Asp Phe Arg		
210	215	220	843
CGA AAG CAC CCC TGG AAC CTT GTT	GCA CTG TCG GTC CTG ACC GCC AGC		
Arg Lys His Pro Trp Asn Leu Val	Ala Leu Ser Val Leu Thr Ala Ser		
225	230	235	891
CTG TCG TAC ATG GTG GGG ATG ATC	GCC AGC TTC TAC AAC ACC GAG GCA		
Leu Ser Tyr Met Val Gly Met Ile	Ala Ser Phe Tyr Asn Thr Glu Ala		
240	245	250	939
GTC ATC ATG GCC GTG GGC ATC ACC	ACA GCC GTC TGC TTC ACC GTC GTC		
Val Ile Met Ala Val Gly Ile Thr	Thr Ala Val Cys Phe Thr Val Val		
255	260	265	987
ATC TTC TCC ATG CAG ACC CGC TAC	GAC TTC ACC TCA TGC ATG GGC GTG		
Ile Phe Ser Met Gln Thr Arg Tyr	Asp Phe Thr Ser Cys Met Gly Val		
270	275	280	1035
CTC CTG GTG AGC ATG GTG GTG CTC	TTC ATC TTC GCC ATT CTC TGC ATC		
Leu Leu Val Ser Met Val Val Leu	Phe Ile Phe Ala Ile Leu Cys Ile		
290	295	300	1083
TTC ATC CGG AAC CGC ATC CTG GAG	ATC GTG TAC GCC TCA CTG GGC GCT		
Phe Ile Arg Asn Arg Ile Leu Glu	Ile Val Tyr Ala Ser Leu Gly Ala		
305	310	315	1131
CTG CTC TTC ACC TGC TTC CTC GCA	GTG GAC ACC CAG CTG CTG CTG GGC		
Leu Leu Phe Thr Cys Phe Leu Ala	Val Asp Thr Gln Leu Leu Leu Gly		
320	325	330	1179
AAC AAG CAG CTG TCC CTG AGC CCA	GAA GAG TAT GTG TTT GCT GCG CTG		
Asn Lys Gln Leu Ser Leu Ser Pro	Glu Glu Tyr Val Phe Ala Ala Leu		
335	340	345	1227
AAC CTG TAC ACA GAC ATC ATC AAC	ATC TTC CTG TAC ATC CTC ACC ATC		
Asn Leu Tyr Thr Asp Ile Ile Asn	Ile Phe Leu Tyr Ile Leu Thr Ile		
350	355	360	1270
ATT GGC CGC GCC AAG GAG TAGCCGAGCT	CCAGCTCGCT GTGCC		
Ile Gly Arg Ala Lys Glu			
370			1330
CGCTCAGGTG GCACGGCTGG CCTGGACCCT	GCCCCTGGCA CGGCAGTGCC AGCTGTACTT		

```

CCCCCTCTCTC TTGTCCCCAG GCACAGCCTA GGGAAAAGGA TGCCTCTCTC CAACCCTCCT 1390
GTATGTACAC TGCAGATACT TCCATTTGGA CCCGCTGTGG CCACAGCATG GCCCCTTTAG 1450
TCCTCCCGCC CCCGCCAAGG GGCACCAAGG CCACGTTTCC GTGCCACCTC CTGTCTACTC 1510
ATTGTTGCAT GAGCCCTGTC TGCCAGCCCA CCCAGGGAC TGGGGGCAGC ACCAGGTCCC 1570
GGGGAGAGGG ATTGAGCCAA GAGGTGAGGG TGCACGTCTT CCCTCCTGTC CCAGCTCCCC 1630
AGCCTGGCGT AGAGCACCCC TCCCCTCCCC CCCACCCCCC TGGAGTGCTG CCCTCTGGGG 1690
ACATGCGGAG TGGGGGTCTT ATCCCTGTGC TGAGCCCTGA GGGCAGAGAG GATGGCATGT 1750
TTCAGGGGAG GGGGAAGCCT TCCTCTCAAT TTGTTGTCAG TGAAATTCCA ATAAATGGGA 1810
TTTGCTCTCT GCCT 1824

```

Sequence No.: 53

Sequence length: 1076

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Stomach cancer

Clone name: HP01098

Sequence characteristics

Code representing characteristics: CDS

Existence site: 62.. 601

Characterization method: E

Sequence description

```

AGTTCCGCCC GCTGGTCATC GCGCCCTTTC CCCTGCCGGT GTCCTGCTCG CCGTCCCCGC 60
C ATG CTG TCT CTA GAC TTT TTG GAC GAT GTG CCG CCG ATG AAC AAG CCG 109
Met Leu Ser Leu Asp Phe Leu Asp Asp Val Arg Arg Met Asn Lys Arg
1 5 10 15
CAG CTC TAT TAT CAA GTC CTA AAT TTT GGA ATG ATT GTC TCA TCG GCA 157
Gln Leu Tyr Tyr Gln Val Leu Asn Phe Gly Met Ile Val Ser Ser Ala
20 25 30
CTA ATG ATC TGG AAG GGG TTA ATG GTA ATA ACT GGA AGT GAA AGT CCG 205
Leu Met Ile Trp Lys Gly Leu Met Val Ile Thr Gly Ser Glu Ser Pro
35 40 45
ATT GTA GTG GTG CTC AGT GGC AGC ATG GAA CCT GCA TTT CAT AGA GGA 253
Ile Val Val Val Leu Ser Gly Ser Met Glu Pro Ala Phe His Arg Gly
50 55 60
GAT CTT CTC TTT CTA ACA AAT CGA GTT GAA GAT CCC ATA CGA GTG GGA 301
Asp Leu Leu Phe Leu Thr Asn Arg Val Glu Asp Pro Ile Arg Val Gly
65 70 75 80
GAA ATT GTT GTT TTT AGG ATA GAA GGA AGA GAG ATT CCT ATA GTT CAC 349

```

WO 98/21328

138

Glu Ile Val Val Phe Arg Ile Glu Gly Arg Glu Ile Pro Ile Val His
 85 90 95
 CGA GTC TTG AAG ATT CAT GAA AAG CAA AAT GGG CAT ATC AAG TTT TTG 397
 Arg Val Leu Lys Ile His Glu Lys Gln Asn Gly His Ile Lys Phe Leu
 100 105 110
 ACC AAA GGA GAT AAT AAT GCG GTT GAT GAC CGA GGC CTC TAT AAA CAA 445
 Thr Lys Gly Asp Asn Asn Ala Val Asp Asp Arg Gly Leu Tyr Lys Gln
 115 120 125
 GGA CAA CAT TGG CTA GAG AAA AAA GAT GTT GTG GGG AGA GCC AGG GGA 493
 Gly Gln His Trp Leu Glu Lys Lys Asp Val Val Gly Arg Ala Arg Gly
 130 135 140
 TTT GTT CCT TAT ATT GGA ATT GTG ACG ATC CTC ATG AAT GAC TAT CCT 541
 Phe Val Pro Tyr Ile Gly Ile Val Thr Ile Leu Met Asn Asp Tyr Pro
 145 150 155 160
 AAA TTT AAG TAT GCA GTT CTC TTT TTG CTG GGT TTA TTC GTG CTG GTT 589
 Lys Phe Lys Tyr Ala Val Leu Phe Leu Leu Gly Leu Phe Val Leu Val
 165 170 175
 CAT CGT GAG TA AGAAGCC TGCCTTGCTG TTCCTGGGAA GAT 630
 His Arg Glu
 GCCATAGTTT TCGTTACTGG ATGTTTGGAG TAGATACTGG TCTGTGATTG GTGGAATGGA 690
 GAACACACGT GTTGGTGCTT CTGGGTAGCA CTGGTTTGCA TTAGTTTATG TTTCCATGCC 750
 AGAGTTTGTG TGGGCGGGCG CATGTGCACC ACAGAGTGCA CTCGAGGGGA CTTTCAGTCA 810
 CAGGATTICA TAATTGTCAT TGTCACACTT TCAAATTTTT GTACATCAGT GAATTTTTTT 870
 ATATTA AAAAG GTTGAGCCAA AGCCCCAGT GTTTGTATTT TGAAGCCAAG CTTCACTTCT 930
 AAAGTGCCTA CAGAGACTTG TAAATGAAAA TGCAGCTCTG CACGAGTTTG AAACCGTCAT 990
 ACCTCCTTCT ATTAGGAATG GCATATACTG AGGTGGTCGT AAGTCTTAAC TTCTAAAATT 1050
 TTAAATAAAA GACTTTGCAC ATTGAG 1076

Sequence No.: 54

Sequence length: 1591

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Liver

Clone name: HP01148

Sequence characteristics

Code representing characteristics: CDS

Existence site: 102.. 1145

Characterization method: E

Sequence description

GTCCCTCCTC TTAACATACT TGCAGCTAAA ACTAAATATT GCTGCTTGGG GACCTCCTTC 60
 TAGCCTTAAA TTTCAGCTCA TCACCTTCAC CTGCCTTGGT C ATG GCT CTG CTA TTC 116
 Met Ala Leu Leu Phe
 1 5
 TCC TTG ATC CTT GCC ATT TGC ACC AGA CCT GGA TTC CTA GCG TCT CCA 164
 Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly Phe Leu Ala Ser Pro
 10 15 20
 TCT GGA GTG CGG CTG GTG GGG GGC CTC CAC CGC TGT GAA GGG CGG GTG 212
 Ser Gly Val Arg Leu Val Gly Gly Leu His Arg Cys Glu Gly Arg Val
 25 30 35
 GAG GTG GAA CAG AAA GGC CAG TGG GGC ACC GTG TGT GAT GAC GGC TGG 260
 Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val Cys Asp Asp Gly Trp
 40 45 50
 GAC ATT AAG GAC GTG GCT GTG TTG TGC CGG GAG CTG GGC TGT GGA GCT 308
 Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu Leu Gly Cys Gly Ala
 55 60 65
 GCC AGC GGA ACC CCT AGT GGT ATT TTG TAT GAG CCA CCA GCA GAA AAA 356
 Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu Pro Pro Ala Glu Lys
 70 75 80 85
 GAG CAA AAG GTC CTC ATC CAA TCA GTC AGT TGC ACA GGA ACA GAA GAT 404
 Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys Thr Gly Thr Glu Asp
 90 95 100
 ACA TTG GCT CAG TGT GAG CAA GAA GAA GTT TAT GAT TGT TCA CAT GAA 452
 Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr Asp Cys Ser His Glu
 105 110 115
 GAA GAT GCT GGG GCA TCG TGT GAG AAC CCA GAG AGC TCT TTC TCC CCA 500
 Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu Ser Ser Phe Ser Pro
 120 125 130
 GTC CCA GAG GGT GTC AGG CTG GCT GAC GGC CCT GGG CAT TGC AAG GGA 548
 Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro Gly His Cys Lys Gly
 135 140 145
 CGC GTG GAA GTG AAG CAC CAG AAC CAG TGG TAT ACC GTG TGC CAG ACA 596
 Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr Thr Val Cys Gln Thr
 150 155 160 165
 GGC TGG AGC CTC CGG GCC GCA AAG GTG GTG TGC CGG CAG CTG GGA TGT 644
 Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys Arg Gln Leu Gly Cys
 170 175 180
 GGG AGG GCT GTA CTG ACT CAA AAA CGC TGC AAC AAG CAT GCC TAT GGC 692
 Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn Lys His Ala Tyr Gly
 185 190 195
 CGA AAA CCC ATC TGG CTG AGC CAG ATG TCA TGC TCA GGA CGA GAA GCA 740
 Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys Ser Gly Arg Glu Ala

140

200	205	210	
ACC CTT CAG GAT TGC CCT TCT GGG CCT TGG GGG AAG AAC ACC TGC AAC			788
Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly Lys Asn Thr Cys Asn			
215	220	225	
CAT GAT GAA GAC ACG TGG GTC GAA TGT GAA GAT CCC TTT GAC TTG AGA			836
His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp Pro Phe Asp Leu Arg			
230	235	240	245
CTA GTA GGA GGA GAC AAC CTC TGC TCT GGG CGA CTG GAG GTG CTG CAC			884
Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg Leu Glu Val Leu His			
250	255	260	
AAG GGC GTA TGG GGC TCT GTC TGT GAT GAC AAC TGG GGA GAA AAG GAG			932
Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn Trp Gly Glu Lys Glu			
265	270	275	
GAC CAG GTG GTA TGC AAG CAA CTG GGC TGT GGG AAG TCC CTC TCT CCC			980
Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly Lys Ser Leu Ser Pro			
280	285	290	
TCC TTC AGA GAC CGG AAA TGC TAT GGC CCT GGG GTT GGC CGC ATC TGG			1028
Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly Val Gly Arg Ile Trp			
295	300	305	
CTG GAT AAT GTT CGT TGC TCA GGG GAG GAG CAG TCC CTG GAG CAG TGC			1076
Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln Ser Leu Glu Gln Cys			
310	315	320	325
CAG CAC AGA TTT TGG GGG TTT CAC GAC TGC ACC CAC CAG GAA GAT GTG			1124
Gln His Arg Phe Trp Gly Phe His Asp Cys Thr His Gln Glu Asp Val			
330	335	340	
GCT GTC ATC TGC TCA GGA TAGTATCCTG GTGTTGCTTG ACCTGGCC			1170
Ala Val Ile Cys Ser Gly			
345			
CCCCCTGGCCC CGCCTGCCCT CTGCTTGTTT TCCTGAGCCC TGATTATCCT CATACTCATT			1230
CTGGGGCTCA GGCTTGAGCC ACTACTCCCT CATCCCCTCA GGAGTCTGAA CACTGGGCTT			1290
ATGCCTTACT CTCAGGGACA AGCAGCCCCC ATTGCTGCCT GTAGATGTGA GCTGTTGAGT			1350
TCCCTCTTGC TGGGGAAGAT GAGCTTCCAT GTATCCTGTG CTCAACCCTG ACCCTTTGAC			1410
ACTGGTTCTG GCCTTTCCTG CCTTTTCTCA AGCTGCCTGG AATCCTCAAA CCTGTCACTT			1470
TGGTCAGATG TGCAGACCAT TACTAAGGTC TATGTCTGCA AACATTACTA ATCTAGGTCC			1530
TATTACTAAT CTATGTCTGC AAACATTAAA GGAATGAAAC AATGAAAGGA ACATTTGAAA			1590
			1591

Sequence No.: 55

Sequence length: 1888

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Liver

Clone name: HP01293

Sequence characteristics

Code representing characteristics: CDS

Existence site: 90.. 1754

Characterization method: E

Sequence description

CCTTTTCAAA GATCTCTGAG GGAGACATTG CACCTGGCCA CTGCAGCCCA GAGCAGGTCT 60
 GGCCACGGCC ATGAGCATGC TGAGCCATC ATG CCC ACC GTG GAT GAC ATT CTG 113
 Met Pro Thr Val Asp Asp Ile Leu
 1 5
 GAG CAG GTT GGG GAG TCT GGC TGG TTC CAG AAG CAA GCC TTC CTC ATC 161
 Glu Gln Val Gly Glu Ser Gly Trp Phe Gln Lys Gln Ala Phe Leu Ile
 10 15 20
 TTA TGC CTG CTG TCG GCT GCC TTT GCG CCC ATC TGT GTG GGC ATC GTC 209
 Leu Cys Leu Leu Ser Ala Ala Phe Ala Pro Ile Cys Val Gly Ile Val
 25 30 35 40
 TTC CTG GGT TTC ACA CCT GAC CAC CAC TGC CAG AGT CCT GGG GTG GCT 257
 Phe Leu Gly Phe Thr Pro Asp His His Cys Gln Ser Pro Gly Val Ala
 45 50 55
 GAG CTG AGC CAG CGC TGT GGC TGG AGC CCT GCG GAG GAG CTG AAC TAT 305
 Glu Leu Ser Gln Arg Cys Gly Trp Ser Pro Ala Glu Glu Leu Asn Tyr
 60 65 70
 ACA GTG CCA GGC CTG GGG CCC GCG GGC GAG GCC TTC CTT GGC CAG TGC 353
 Thr Val Pro Gly Leu Gly Pro Ala Gly Glu Ala Phe Leu Gly Gln Cys
 75 80 85
 AGG CGC TAT GAA GTG GAC TGG AAC CAG AGC GCC CTC AGC TGT GTA GAC 401
 Arg Arg Tyr Glu Val Asp Trp Asn Gln Ser Ala Leu Ser Cys Val Asp
 90 95 100
 CCC CTG GCT AGC CTG GCC ACC AAC AGG AGC CAC CTG CCG CTG GGT CCC 449
 Pro Leu Ala Ser Leu Ala Thr Asn Arg Ser His Leu Pro Leu Gly Pro
 105 110 115 120
 TGC CAG GAT GGC TGG GTG TAT GAC ACG CCC GGC TCT TCC ATC GTC ACT 497
 Cys Gln Asp Gly Trp Val Tyr Asp Thr Pro Gly Ser Ser Ile Val Thr
 125 130 135
 GAG TTC AAC CTG GTG TGT GCT GAC TCC TGG AAG CTG GAC CTC TTT CAG 545
 Glu Phe Asn Leu Val Cys Ala Asp Ser Trp Lys Leu Asp Leu Phe Gln
 140 145 150
 TCC TGT TTG AAT GCG GGC TTC TTC TTT GGC TCT CTC GGT GTT GGC TAC 593
 Ser Cys Leu Asn Ala Gly Phe Phe Phe Gly Ser Leu Gly Val Gly Tyr
 155 160 165

142

TTT GCA GAC AGG TTT GGC CGT AAG CTG TGT CTC CTG GGA ACT GTG CTG 641
 Phe Ala Asp Arg Phe Gly Arg Lys Leu Cys Leu Leu Gly Thr Val Leu
 170 175 180
 GTC AAC GCG GTG TCG GGC GTG CTC ATG GCC TTC TCG CCC AAC TAC ATG 689
 Val Asn Ala Val Ser Gly Val Leu Met Ala Phe Ser Pro Asn Tyr Met
 185 190 195 200
 TCC ATG CTG CTC TTC CGC CTG CTG CAG GGC CTG GTC AGC AAG GGC AAC 737
 Ser Met Leu Leu Phe Arg Leu Leu Gln Gly Leu Val Ser Lys Gly Asn
 205 210 215
 TGG ATG GCT GGC TAC ACC CTA ATC ACA GAA TTT GTT GGC TCG GGC TCC 785
 Trp Met Ala Gly Tyr Thr Leu Ile Thr Glu Phe Val Gly Ser Gly Ser
 220 225 230
 AGA AGA ACG GTG GCG ATC ATG TAC CAG ATG GCC TTC ACG GTG GGC CTG 833
 Arg Arg Thr Val Ala Ile Met Tyr Gln Met Ala Phe Thr Val Gly Leu
 235 240 245
 GTG GCG CTT ACC GGG CTG GCC TAC GCC CTG CCT CAC TGG CGC TGG CTG 881
 Val Ala Leu Thr Gly Leu Ala Tyr Ala Leu Pro His Trp Arg Trp Leu
 250 255 260
 CAG CTG GCA GTC TCC CTG CCC ACC TTC CTC TTC CTG CTC TAC TAC TGG 929
 Gln Leu Ala Val Ser Leu Pro Thr Phe Leu Phe Leu Leu Tyr Tyr Trp
 265 270 275 280
 TGT GTG CCG GAG TCC CCT CGG TGG CTG TTA TCA CAA AAA AGA AAC ACT 977
 Cys Val Pro Glu Ser Pro Arg Trp Leu Leu Ser Gln Lys Arg Asn Thr
 285 290 295
 GAA GCA ATA AAG ATA ATG GAC CAC ATC GCT CAA AAG AAT GGC AAG TTG 1025
 Glu Ala Ile Lys Ile Met Asp His Ile Ala Gln Lys Asn Gly Lys Leu
 300 305 310
 CCT CCT GCT GAT TTA AAG ATG CTT TCC CTC GAA GAG GAT GTC ACC GAA 1073
 Pro Pro Ala Asp Leu Lys Met Leu Ser Leu Glu Glu Asp Val Thr Glu
 315 320 325
 AAG CTG AGC CCT TCA TTT GCA GAC CTG TTC CGC ACG CCG CGC CTG AGG 1121
 Lys Leu Ser Pro Ser Phe Ala Asp Leu Phe Arg Thr Pro Arg Leu Arg
 330 335 340
 AAG CGC ACC TTC ATC CTG ATG TAC CTG TGG TTC ACG GAC TCT GTG CTC 1169
 Lys Arg Thr Phe Ile Leu Met Tyr Leu Trp Phe Thr Asp Ser Val Leu
 345 350 355 360
 TAT CAG GGG CTC ATC CTG CAC ATG GGC GCC ACC AGC GGG AAC CTC TAC 1217
 Tyr Gln Gly Leu Ile Leu His Met Gly Ala Thr Ser Gly Asn Leu Tyr
 365 370 375
 CTG GAT TTC CTT TAC TCC GCT CTG GTC GAA ATC CCG GGG GCC TTC ATA 1265
 Leu Asp Phe Leu Tyr Ser Ala Leu Val Glu Ile Pro Gly Ala Phe Ile
 380 385 390
 GCC CTC ATC ACC ATT GAC CGC GTG GGC CGC ATC TAC CCC ATG GCC GTG 1313
 Ala Leu Ile Thr Ile Asp Arg Val Gly Arg Ile Tyr Pro Met Ala Val

143

395	400	405	
TCA AAT TTG TTG GCG GGG GCA GCC TGC CTC GTC ATG ATT TTT ATC TCA			1361
Ser Asn Leu Leu Ala Gly Ala Ala Cys Leu Val Met Ile Phe Ile Ser			
410	415	420	
CCT GAC CTG CAC TGG TTA AAC ATC ATA ATC ATG TGT GTT GGC CGA ATG			1409
Pro Asp Leu His Trp Leu Asn Ile Ile Ile Met Cys Val Gly Arg Met			
425	430	435	440
GGA ATC ACC ATT GCA ATA CAA ATG ATC TGC CTG GTG AAT GCT GAG CTG			1457
Gly Ile Thr Ile Ala Ile Gln Met Ile Cys Leu Val Asn Ala Glu Leu			
445	450	455	
TAC CCC ACA TTC GTC AGG AAC CTC GGA GTG ATG GTG TGT TCC TCC CTG			1505
Tyr Pro Thr Phe Val Arg Asn Leu Gly Val Met Val Cys Ser Ser Leu			
460	465	470	
TGT GAC ATA GGT GGG ATA ATC ACC CCC TTC ATA GTC TTC AGG CTG AGG			1553
Cys Asp Ile Gly Gly Ile Ile Thr Pro Phe Ile Val Phe Arg Leu Arg			
475	480	485	
GAG GTC TGG CAA GCC TTG CCC CTC ATT TTG TTT GCG GTG TTG GGC CTG			1601
Glu Val Trp Gln Ala Leu Pro Leu Ile Leu Phe Ala Val Leu Gly Leu			
490	495	500	
CTT GCC GCG GGA GTG ACG CTA CTT CTT CCA GAG ACC AAG GGG GTC GCT			1649
Leu Ala Ala Gly Val Thr Leu Leu Leu Pro Glu Thr Lys Gly Val Ala			
505	510	515	520
TTG CCA GAG ACC ATG AAG GAC GCC GAG AAC CTT GGG AGA AAA GCA AAG			1697
Leu Pro Glu Thr Met Lys Asp Ala Glu Asn Leu Gly Arg Lys Ala Lys			
525	530	535	
CCC AAA GAA AAC ACG ATT TAC CTT AAG GTC CAA ACC TCA GAA CCC TCG			1745
Pro Lys Glu Asn Thr Ile Tyr Leu Lys Val Gln Thr Ser Glu Pro Ser			
540	545	550	
GGC ACC TGAGAGAGAT GTTTTGC GGC GATGTCGTGT TGGAGGGATG AAGATGGAG			1800
Gly Thr			
TTATCCTCTG CAGAAATTCC TAGACGCCTT CACTTCTCTG TATTCTTCCT CATACTTGCC			1860
TACCCCAAAA TTAATATCAG TCCTAAAG			1888

Sequence No.: 56

Sequence length: 2033

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Epidermoid carcinoma

Cell line: KB
 Clone name: HP10013
 Sequence characteristics
 Code representing characteristics: CDS
 Existence site: 97.. 1149
 Characterization method: E
 Sequence description

GAGTCCGAGC GCGTCACCTC CTCACGCTGC GGCTGTCGCC CGTGTCCCGC CGGCCCGTTC 60
 CGTGTGCGCC CGCAGTGCTG CGGCCGCGCC GGCACC ATG GCT GTG TTT GTC GTG 114
 Met Ala Val Phe Val Val
 1 5
 CTC CTG GCG TTG GTG GCG GGT GTT TTG GGG AAC GAG TTT AGT ATA TTA 162
 Leu Leu Ala Leu Val Ala Gly Val Leu Gly Asn Glu Phe Ser Ile Leu
 10 15 20
 AAA TCA CCA GGG TCT GTT GTT TTC CGA AAT GGA AAT TGG CCT ATA CCA 210
 Lys Ser Pro Gly Ser Val Val Phe Arg Asn Gly Asn Trp Pro Ile Pro
 25 30 35
 GGA GAG CGG ATC CCA GAC GTG GCT GCA TTG TCC ATG GGC TTC TCT GTG 258
 Gly Glu Arg Ile Pro Asp Val Ala Ala Leu Ser Met Gly Phe Ser Val
 40 45 50
 AAA GAA GAC CTT TCT TGG CCA GGA CTC GCA GTG GGT AAC CTG TTT CAT 306
 Lys Glu Asp Leu Ser Trp Pro Gly Leu Ala Val Gly Asn Leu Phe His
 55 60 65 70
 CGT CCT CGG GCT ACC GTC ATG GTG ATG GTG AAG GGA GTG AAC AAA CTG 354
 Arg Pro Arg Ala Thr Val Met Val Met Val Lys Gly Val Asn Lys Leu
 75 80 85
 GCT CTA CCC CCA GGC AGT GTC ATT TCG TAC CCT TTG GAG AAT GCA GTT 402
 Ala Leu Pro Pro Gly Ser Val Ile Ser Tyr Pro Leu Glu Asn Ala Val
 90 95 100
 CCT TTT AGT CTT GAC AGT GTT GCA AAT TCC ATT CAC TCC TTA TTT TCT 450
 Pro Phe Ser Leu Asp Ser Val Ala Asn Ser Ile His Ser Leu Phe Ser
 105 110 115
 GAG GAA ACT CCT GTT GTT TTG CAG TTG GCT CCC AGT GAG GAA AGA GTG 498
 Glu Glu Thr Pro Val Val Leu Gln Leu Ala Pro Ser Glu Glu Arg Val
 120 125 130
 TAT ATG GTA GGG AAG GCA AAC TCA GTG TTT GAA GAC CTT TCA GTC ACC 546
 Tyr Met Val Gly Lys Ala Asn Ser Val Phe Glu Asp Leu Ser Val Thr
 135 140 145 150
 TTG CGC CAG CTC CGT AAT CGC CTG TTT CAA GAA AAC TCT GTT CTC AGT 594
 Leu Arg Gln Leu Arg Asn Arg Leu Phe Gln Glu Asn Ser Val Leu Ser
 155 160 165
 TCA CTC CCC CTC AAT TCT CTG AGT AGG AAC AAT GAA GTT GAC CTG CTC 642
 Ser Leu Pro Leu Asn Ser Leu Ser Arg Asn Asn Glu Val Asp Leu Leu

145
170 175 180
TTT CTT TCT GAA CTG CAA GTG CTA CAT GAT ATT TCA AGC TTG CTG TCT 690
Phe Leu Ser Glu Leu Gln Val Leu His Asp Ile Ser Ser Leu Leu Ser
185 190 195
CGT CAT AAG CAT CTA GCC AAG GAT CAT TCT CCT GAT TTA TAT TCA CTG 738
Arg His Lys His Leu Ala Lys Asp His Ser Pro Asp Leu Tyr Ser Leu
200 205 210
GAG CTG GCA GGT TTG GAT GAA ATT GGG AAG CGT TAT GGG GAA GAC TCT 786
Glu Leu Ala Gly Leu Asp Glu Ile Gly Lys Arg Tyr Gly Glu Asp Ser
215 220 225 230
GAA CAA TTC AGA GAT GCT TCT AAG ATC CTT GTT GAC GCT CTG CAA AAG 834
Glu Gln Phe Arg Asp Ala Ser Lys Ile Leu Val Asp Ala Leu Gln Lys
235 240 245
TTT GCA GAT GAC ATG TAC AGT CTT TAT GGT GGG AAT GCA GTG GTA GAG 882
Phe Ala Asp Asp Met Tyr Ser Leu Tyr Gly Gly Asn Ala Val Val Glu
250 255 260
TTA GTC ACT GTC AAG TCA TTT GAC ACC TCC CTC ATT AGG AAG ACA AGG 930
Leu Val Thr Val Lys Ser Phe Asp Thr Ser Leu Ile Arg Lys Thr Arg
265 270 275
ACT ATC CTT GAG GCA AAA CAA GCG AAG AAC CCA GCA AGT CCC TAT AAC 978
Thr Ile Leu Glu Ala Lys Gln Ala Lys Asn Pro Ala Ser Pro Tyr Asn
280 285 290
CTT GCA TAT AAG TAT AAT TTT GAA TAT TCC GTG GTT TTC AAC ATG GTA 1026
Leu Ala Tyr Lys Tyr Asn Phe Glu Tyr Ser Val Val Phe Asn Met Val
295 300 305 310
CTT TGG ATA ATG ATC GCC TTG GCC TTG GCT GTG ATT ATC ACC TCT TAC 1074
Leu Trp Ile Met Ile Ala Leu Ala Leu Ala Val Ile Ile Thr Ser Tyr
315 320 325
AAT ATT TGG AAC ATG GAT CCT GGA TAT GAT AGC ATC ATT TAT AGG ATG 1122
Asn Ile Trp Asn Met Asp Pro Gly Tyr Asp Ser Ile Ile Tyr Arg Met
330 335 340
ACA AAC CAG AAG ATT CGA ATG GAT TGAATGTTAC CTGTGCCAGA ATTA 1170
Thr Asn Gln Lys Ile Arg Met Asp
345 350
GAAAAGGGGG TTGGAAATTG GCTGTTTTGT TAAAAATATAT CTTTTAGTGT GCTTTAAAGT 1230
AGATAGTATA CTTTACATTT ATAAAAAAA ATCAAATTTT GTTCTTTATT TTGTGTGTGC 1290
CTGTGATGTT TTTCTAGAGT GAATTATAGT ATTGACGTGA ATCCCACTGT GGTATAGATT 1350
CCATAATATG CTTGAATATT ATGATATAGC CATTTAATAA CATTGATTTT ATTCTGTTTA 1410
ATGAATTTGG AAATATGCAC TGAAAGAAAT GTAAACATT TAGAATAGCT CGTGTATG 1470
AAAAAGTGC ACTGAATTTA TTAGACAAAC TTACGAATGC TTAACCTCTT TACACAGCAT 1530
AGGTGAAAAT CATATTTGGG CTATTGTATA CTATGAACAA TTTGTAAATG TCTTAATTTG 1590
ATGTAAATAA CTCTGAAACA AGAGAAAAGG TTTTAACTT AGAGTAGCCC TAAAAATATG 1650
ATGTGCTTAT ATAATCGCTT AGTTTTGGAA CTGTATCTGA GTAACAGAGG ACAGCTGTTT 1710
TTTAACCTC TTCTGCAAGT TTGTTGACCT ACATGGGCTA ATATGGATAC TAAAAATACT 1770

ACATTGATCT AAGAAGAAAC TAGCCTTGTG GAGTATATAG ATGCTTTTCA TTATACACAC 1830
 AAAAATCCCT GAGGGACATT TTGAGGCATG AATATAAAAC ATTTTATTT CAGTAACTTT 1890
 TCCCCCTGTG TAAGTTACTA TGGTTTGTGG TACAACTTCA TTCTATAGAA TATTAAGTGG 1950
 AAGTGGGTGA ATTCTACTTT TTATGTTGGA GTGGACCAAT GTCTATCAAG AGTGACAAAT 2010
 AAAGTTAATG ATGATTCCAA AAC 2033

Sequence No.: 57

Sequence length: 911

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Fibrosarcoma

Cell line: HT-1080

Clone name: HP10034

Sequence characteristics

Code representing characteristics: CDS

Existence site: 176.. 805

Characterization method: E

Sequence description

ACGCCTGGGT GACCTCTACG TATATACAGA GCCTCCCTGG CCCTCCTGGA AAGAGTCCTG 60
 GAAAGACAAC CTCAGGTCC AGCCCTGGAG CTGGAGGAGT GGAGCCCCAC TCTGAAGACG 120
 CAGCCTTTCT CCAGGTTCTG TCTCTCCCAT TCTGATTCTT GACACCAGAT GCAGG ATG 178
 Met
 1
 GTG TCC TCT CCC TGC ACG CAG GCA AGC TCA CGG ACT TGC TCC CGT ATC 226
 Val Ser Ser Pro Cys Thr Gln Ala Ser Ser Arg Thr Cys Ser Arg Ile
 5 10 15
 CTG GGA CTG AGC CTT GGG ACT GCA GCC CTG TTT GCT GCT GGG GCC AAC 274
 Leu Gly Leu Ser Leu Gly Thr Ala Ala Leu Phe Ala Ala Gly Ala Asn
 20 25 30
 GTG GCA CTC CTC CTT CCT AAC TGG GAT GTC ACC TAC CTG TTG AGG GGC 322
 Val Ala Leu Leu Leu Pro Asn Trp Asp Val Thr Tyr Leu Leu Arg Gly
 35 40 45
 CTC CTT GGC AGG CAT GCC ATG CTG GGA ACT GGG CTC TGG GGA GGA GGC 370
 Leu Leu Gly Arg His Ala Met Leu Gly Thr Gly Leu Trp Gly Gly Gly
 50 55 60 65
 CTC ATG GTA CTC ACT GCA GCT ATC CTC ATC TCC TTG ATG GGC TGG AGA 418
 Leu Met Val Leu Thr Ala Ala Ile Leu Ile Ser Leu Met Gly Trp Arg

147

70	75	80	
TAC GGC TGC TTC AGT AAG AGT GGG CTC TGT CGA AGC GTG CTT ACT GCT			466
Tyr Gly Cys Phe Ser Lys Ser Gly Leu Cys Arg Ser Val Leu Thr Ala			
85	90	95	
CTG TTG TCA GGT GGC CTG GCT TTA CTT GGA GCC CTG ATT TGC TTT GTC			514
Leu Leu Ser Gly Gly Leu Ala Leu Leu Gly Ala Leu Ile Cys Phe Val			
100	105	110	
ACT TCT GGA GTT GCT CTG AAA GAT GGT CCT TTT TGC ATG TTT GAT GTT			562
Thr Ser Gly Val Ala Leu Lys Asp Gly Pro Phe Cys Met Phe Asp Val			
115	120	125	
TCA TCC TTC AAT CAG ACA CAA GCT TGG AAA TAT GGT TAC CCA TTC AAA			610
Ser Ser Phe Asn Gln Thr Gln Ala Trp Lys Tyr Gly Tyr Pro Phe Lys			
130	135	140	
GAC CTG CAT AGT AGG AAT TAT CTG TAT GAC CGT TCG CTC TGG AAC TCC			658
Asp Leu His Ser Arg Asn Tyr Leu Tyr Asp Arg Ser Leu Trp Asn Ser			
150	155	160	
GTC TGC CTG GAG CCC TCT GCA GCT GTT GTC TGG CAC GTG TCC CTC TTC			706
Val Cys Leu Glu Pro Ser Ala Ala Val Val Trp His Val Ser Leu Phe			
165	170	175	
TCC GCC CTT CTG TGC ATC AGC CTG CTC CAG CTT CTC CTG GTG GTC GTT			754
Ser Ala Leu Leu Cys Ile Ser Leu Leu Gln Leu Leu Leu Val Val Val			
180	185	190	
CAT GTC ATC AAC AGC CTC CTG GGC CTT TTC TGC AGC CTC TGC GAG AAG			802
His Val Ile Asn Ser Leu Leu Gly Leu Phe Cys Ser Leu Cys Glu Lys			
195	200	205	
TGACAGGC AGAACCTTCA CTTGCAAGCA TGGGTGTTTA TCATCATCGG CTGTCTTGAA			860
TCCTTTCTAC AAGGAGTGGG TACGAATTAT AAACAACTT CCCCTTTAGG T			911

Sequence No.: 58

Sequence length: 601

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Fibrosarcoma

Cell line: HT-1080

Clone name: HP10050

Sequence characteristics

Code representing characteristics: CDS

Existence site: 10.. 501

Characterization method: E

148

Sequence description

CCATCTGTC ATG GCG GCT GGG CTG TTT GGT TTG AGC GCT CGC CGT CTT TTG 51
 Met Ala Ala Gly Leu Phe Gly Leu Ser Ala Arg Arg Leu Leu
 1 5 10
 GCG GCA GCG GCG ACG CGA GGG CTC CCG GCC GCC CGC GTC CGC TGG GAA 99
 Ala Ala Ala Ala Thr Arg Gly Leu Pro Ala Ala Arg Val Arg Trp Glu
 15 20 25 30
 TCT AGC TTC TCC AGG ACT GTG GTC GCC CCG TCC GCT GTG GCG GGA AAG 147
 Ser Ser Phe Ser Arg Thr Val Val Ala Pro Ser Ala Val Ala Gly Lys
 35 40 45
 CGG CCC CCA GAA CCG ACC ACA CCG TGG CAA GAG GAC CCA GAA CCC GAG 195
 Arg Pro Pro Glu Pro Thr Thr Pro Trp Gln Glu Asp Pro Glu Pro Glu
 50 55 60
 GAC GAA AAC TTG TAT GAG AAG AAC CCA GAC TCC CAT GGT TAT GAC AAG 243
 Asp Glu Asn Leu Tyr Glu Lys Asn Pro Asp Ser His Gly Tyr Asp Lys
 65 70 75
 GAC CCC GTT TTG GAC GTC TGG AAC ATG CGA CTT GTC TTC TTC TTT GGC 291
 Asp Pro Val Leu Asp Val Trp Asn Met Arg Leu Val Phe Phe Phe Gly
 80 85 90
 GTC TCC ATC ATC CTG GTC CTT GGC AGC ACC TTT GTG GCC TAT CTG CCT 339
 Val Ser Ile Ile Leu Val Leu Gly Ser Thr Phe Val Ala Tyr Leu Pro
 95 100 105 110
 GAC TAC AGG TGC ACA GGG TGT CCA AGA GCG TGG GAT GGG ATG AAA GAG 387
 Asp Tyr Arg Cys Thr Gly Cys Pro Arg Ala Trp Asp Gly Met Lys Glu
 115 120 125
 TGG TCC CGC CGC GAA GCT GAG AGG CTT GTG AAA TAC CGA GAG GCC AAT 435
 Trp Ser Arg Arg Glu Ala Glu Arg Leu Val Lys Tyr Arg Glu Ala Asn
 130 135 140
 GGC CTT CCC ATC ATG GAA TCC AAC TGC TTC GAC CCC AGC AAG ATC CAG 483
 Gly Leu Pro Ile Met Glu Ser Asn Cys Phe Asp Pro Ser Lys Ile Gln
 145 150 155
 CTG CCA GAG GAT GAG TGACCAGTTG CTAAGTGGGG CTCAAGAAGC AC 530
 Leu Pro Glu Asp Glu
 160
 CGCCTTCCCC ACCCCCTGCC TGCCATTCTG ACCTCTTCTC AGAGCACCTA ATTAAAGGGG 590
 CTGAAAGTCT G 601

Sequence No.: 59

Sequence length: 394

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Stomach cancer

Clone name: HP10071

Sequence characteristics

Code representing characteristics: CDS

Existence site: 47.. 325

Characterization method: E

Sequence description

```

AACATCCGGG CCGCGCGGGG AAGGGGAGAC GTGGGGTAGA GTGACC ATG ACG AAA      55
                                         Met Thr Lys
                                         1
TTA GCG CAG TGG CTT TGG GGA CTA GCG ATC CTG GGC TCC ACC TGG GTG      103
Leu Ala Gln Trp Leu Trp Gly Leu Ala Ile Leu Gly Ser Thr Trp Val
      5              10              15
GCC CTG ACC ACG GGA GCC TTG GGC CTG GAG CTG CCC TTG TCC TGC CAG      151
Ala Leu Thr Thr Gly Ala Leu Gly Leu Glu Leu Pro Leu Ser Cys Gln
      20              25              30              35
GAA GTC CTG TGG CCA CTG CCC GCC TAC TTG CTG GTG TCC GCC GGC TGC      199
Glu Val Leu Trp Pro Leu Pro Ala Tyr Leu Leu Val Ser Ala Gly Cys
      40              45              50
TAT GCC CTG GGC ACT GTG GGC TAT CGT GTG GCC ACT TTT CAT GAC TGC      247
Tyr Ala Leu Gly Thr Val Gly Tyr Arg Val Ala Thr Phe His Asp Cys
      55              60              65
GAG GAC GCC GCA CGC GAG CTG CAG AGC CAG ATA CAG GAG GCC CGA GCC      295
Glu Asp Ala Ala Arg Glu Leu Gln Ser Gln Ile Gln Glu Ala Arg Ala
      70              75              80
GAC TTA GCC CGC AGG GGG CTG CGC TTC TGACAGCCTA ACCCCATT      340
Asp Leu Ala Arg Arg Gly Leu Arg Phe
      85              90
CCTGTGCGGA CAGCCCTTCC TCCCATTTCC CATTAAAGAG CCAGTTTATT TTCT      394

```

Sequence No.: 60

Sequence length: 732

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Lymphoma

Cell line: U937

Clone name: HP10076

Sequence characteristics

Code representing characteristics: CDS

Existence site: 82.. 600

Characterization method: E

Sequence description

AGAAACGTGT TCGCTGCCCA GAAGAAGGGA AGGCGCGAGT GAGGAAAGGA GGTACTGTAG 60
 ATGCCCTCCA AATCCTTGGT T ATG GAA TAT TTG GCT CAT CCC AGT ACA CTC 111
 Met Glu Tyr Leu Ala His Pro Ser Thr Leu
 1 5 10
 GGC TTG GCT GTT GGA GTT GCT TGT GGC ATG TGC CTG GGC TGG AGC CTT 159
 Gly Leu Ala Val Gly Val Ala Cys Gly Met Cys Leu Gly Trp Ser Leu
 15 20 25
 CGA GTA TGC TTT GGG ATG CTC CCC AAA AGC AAG ACG AGC AAG ACA CAC 207
 Arg Val Cys Phe Gly Met Leu Pro Lys Ser Lys Thr Ser Lys Thr His
 30 35 40
 ACA GAT ACT GAA AGT GAA GCA AGC ATC TTG GGA GAC AGC GGG GAG TAC 255
 Thr Asp Thr Glu Ser Glu Ala Ser Ile Leu Gly Asp Ser Gly Glu Tyr
 45 50 55
 AAG ATG ATT CTT GTG GTT CGA AAT GAC TTA AAG ATG GGA AAA GGG AAA 303
 Lys Met Ile Leu Val Val Arg Asn Asp Leu Lys Met Gly Lys Gly Lys
 60 65 70
 GTG GCT GCC CAG TGC TCT CAT GCT GCT GTT TCA GCC TAC AAG CAG ATT 351
 Val Ala Ala Gln Cys Ser His Ala Ala Val Ser Ala Tyr Lys Gln Ile
 75 80 85 90
 CAA AGA AGA AAT CCT GAA ATG CTC AAA CAA TGG GAA TAC TGT GGC CAG 399
 Gln Arg Arg Asn Pro Glu Met Leu Lys Gln Trp Glu Tyr Cys Gly Gln
 95 100 105
 CCC AAG GTG GTG GTC AAA GCT CCT GAT GAA GAA ACC CTG ATT GCA TTA 447
 Pro Lys Val Val Val Lys Ala Pro Asp Glu Glu Thr Leu Ile Ala Leu
 110 115 120
 TTG GCC CAT GCA AAA ATG CTG GGA CTG ACT GTA AGT TTA ATT CAA GAT 495
 Leu Ala His Ala Lys Met Leu Gly Leu Thr Val Ser Leu Ile Gln Asp
 125 130 135
 GCT GGA CGT ACT CAG ATT GCA CCA GGC TCT CAA ACT GTC CTA GGG ATT 543
 Ala Gly Arg Thr Gln Ile Ala Pro Gly Ser Gln Thr Val Leu Gly Ile
 140 145 150
 GGG CCA GGA CCA GCA GAC CTA ATT GAC AAA GTC ACT GGT CAC CTA AAA 591
 Gly Pro Gly Pro Ala Asp Leu Ile Asp Lys Val Thr Gly His Leu Lys
 155 160 165 170
 CTT TAC TAGGTGGACT TTGATATGAC AACAAACCCT CCATCACAAG TGT 640
 Leu Tyr

TTGAAGCCTG TCAGATTCTA ACAACAAAAG CTGAATTTCT TCACCCAAC TAAATGTTCT 700
 TGAGATGAAA ATAAACCTA TTCCCATGTT CT 732

Sequence No.: 61
 Sequence length: 697
 Sequence type: Nucleic acid
 Strandedness: Double
 Topology: Linear
 Sequence kind: cDNA to mRNA
 Original source:

Organism species: *Homo sapiens*

Cell kind: Lymphoma

Cell line: U937

Clone name: HP10085

Sequence characteristics

Code representing characteristics: CDS

Existence site: 151.. 600

Characterization method: E

Sequence description

TATACCTCTA GTTGGAGCT GTGCTGTAAA AACAAGAGTA ACATTTTAT ATTAAAGTTA 60
 AATAAGTTA CAACTTTGAA GAGAGTTTCT GCAAGACATG ACACAAAGCT GCTAGCAGAA 120
 AATCAAAACG CTGATTAAAA GAAGCACGGT ATG ATG ACC AAA CAT AAA AAG TGT 174
 Met Met Thr Lys His Lys Lys Cys
 1 5
 TTT ATA ATT GTT GGT GTT TTA ATA ACA ACT AAT ATT ATT ACT CTG ATA 222
 Phe Ile Ile Val Gly Val Leu Ile Thr Thr Asn Ile Ile Thr Leu Ile
 10 15 20
 GTT AAA CTA ACT CGA GAT TCT CAG AGT TTA TGC CCC TAT GAT TGG ATT 270
 Val Lys Leu Thr Arg Asp Ser Gln Ser Leu Cys Pro Tyr Asp Trp Ile
 25 30 35 40
 GGT TTC CAA AAC AAA TGC TAT TAT TTC TCT AAA GAA GAA GGA GAT TGG 318
 Gly Phe Gln Asn Lys Cys Tyr Tyr Phe Ser Lys Glu Glu Gly Asp Trp
 45 50 55
 AAT TCA AGT AAA TAC AAC TGT TCC ACT CAA CAT GCC GAC CTA ACT ATA 366
 Asn Ser Ser Lys Tyr Asn Cys Ser Thr Gln His Ala Asp Leu Thr Ile
 60 65 70
 ATT GAC AAC ATA GAA GAA ATG AAT TTT CTT AGG CGG TAT AAA TGC AGT 414
 Ile Asp Asn Ile Glu Glu Met Asn Phe Leu Arg Arg Tyr Lys Cys Ser
 75 80 85
 TCT GAT CAC TGG ATT GGA CTG AAG ATG GCA AAA AAT CGA ACA GGA CAA 462
 Ser Asp His Trp Ile Gly Leu Lys Met Ala Lys Asn Arg Thr Gly Gln

152

90	95	100	510
TGG GTA GAT GGA GCT ACA TTT ACC AAA TCG TTT GGC ATG AGA GGG AGT			
Trp Val Asp Gly Ala Thr Phe Thr Lys Ser Phe Gly Met Arg Gly Ser			
105	110	115	120
GAA GGA TGT GCC TAC CTC AGC GAT GAT GGT GCA GCA ACA GCT AGA TGT			558
Glu Gly Cys Ala Tyr Leu Ser Asp Asp Gly Ala Ala Thr Ala Arg Cys			
125	130	135	
TAC ACC GAA AGA AAA TGG ATT TGC AGG AAA AGA ATA CAC TAA			600
Tyr Thr Glu Arg Lys Trp Ile Cys Arg Lys Arg Ile His			
140	145		
GTTAATGTCT AAGATAATGG GGAAAATAGA AAATAACATT ATTAAGTGTA AAACCAGCAA			660
AGTACTTTTT TAATTAAACA AAGTTCGAGT TTTGTAC			697

Sequence No.: 62

Sequence length: 1186

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Stomach cancer

Clone name: HP10122

Sequence characteristics

Code representing characteristics: CDS

Existence site: 139.. 705

Characterization method: E

Sequence description

AAGTGCGATC TTCGGGCTGT CAGAGTTGGT CTGTTACTCG GTGGTGGCGG AGTCTACGGA	60
AGCCGTTTTTC GCTTCACTTT TCCTGGCTGT AGAGCGCTTT CCCCCTGGCG GGTGAGAGTG	120
CAGAGACGAA GGTGCGAG ATG AGC ACT ATG TTC GCG GAC ACT CTC CTC ATC	171
Met Ser Thr Met Phe Ala Asp Thr Leu Leu Ile	
1 5 10	
GTT TTT ATC TCT GTG TGC ACG GCT CTG CTC GCA GAG GGC ATA ACC TGG	219
Val Phe Ile Ser Val Cys Thr Ala Leu Leu Ala Glu Gly Ile Thr Trp	
15 20 25	
GTC CTG GTT TAC AGG ACA GAC AAG TAC AAG AGA CTG AAG GCA GAA GTG	267
Val Leu Val Tyr Arg Thr Asp Lys Tyr Lys Arg Leu Lys Ala Glu Val	
30 35 40	
GAA AAA CAG AGT AAA AAA TTG GAA AAG AAG AAG GAA ACA ATA ACA GAG	315
Glu Lys Gln Ser Lys Lys Leu Glu Lys Lys Lys Glu Thr Ile Thr Glu	
45 50 55	

153

TCA GCT GGT CGA CAA CAG AAA AAG AAA ATA CAG AGA CAA GAA GAG AAA 363
 Ser Ala Gly Arg Gln Gln Lys Lys Lys Ile Glu Arg Gln Glu Glu Lys
 60 65 70 75
 CTG AAG AAT AAC AAC AGA GAT CTA TCA ATG GTT CGA ATG AAA TCC ATG 411
 Leu Lys Asn Asn Asn Arg Asp Leu Ser Met Val Arg Met Lys Ser Met
 80 85 90
 TTT GCT ATT GGC TTT TGT TTT ACT GCC CTA ATG GGA ATG TTC AAT TCC 459
 Phe Ala Ile Gly Phe Cys Phe Thr Ala Leu Met Gly Met Phe Asn Ser
 95 100 105
 ATA TTT GAT GGT AGA GTG GTG GCA AAG CTT CCT TTT ACC CCT CTT TCT 507
 Ile Phe Asp Gly Arg Val Val Ala Lys Leu Pro Phe Thr Pro Leu Ser
 110 115 120
 TAC ATC CAA GGA CTG TCT CAT CGA AAT CTG CTG GGA GAT GAC ACC ACA 555
 Tyr Ile Gln Gly Leu Ser His Arg Asn Leu Leu Gly Asp Asp Thr Thr
 125 130 135
 GAC TGT TCC TTC ATT TTC CTG TAT ATT CTC TGT ACT ATG TCG ATT CGA 603
 Asp Cys Ser Phe Ile Phe Leu Tyr Ile Leu Cys Thr Met Ser Ile Arg
 140 145 150 155
 CAG AAC ATT CAG AAG ATT CTC GGC CTT GCC CCT TCA CGA GCC GCC ACC 651
 Gln Asn Ile Gln Lys Ile Leu Gly Leu Ala Pro Ser Arg Ala Ala Thr
 160 165 170
 AAG CAG GCA GGT GGA TTT CTT GGC CCA CCA CCT CCT TCT GGG AAG TTC 699
 Lys Gln Ala Gly Gly Phe Leu Gly Pro Pro Pro Pro Ser Gly Lys Phe
 175 180 185
 TCT TGA ACT CAAG AACTCTTTAT TTTCTATCAT TCTTTCTAGA CACACACA 750
 Ser
 CATCAGACTG GCAACTGTTT TG TAGCAAGA GCCATAGGTA GCCTTACTAC TTGGGCCTCT 810
 TTCTAGTTTT GAATTATTTT TAAGCCTTTT GGGTATGATT AGAGTGAAAA TGGCAGCCAG 870
 CAAACTTGAT AGTGCTTTTG GTCCTAGATG ATTTTATCA AATAAGTGGA TTGATTAGTT 930
 AAGTTCAGGT AATGTTTATG TAATGAAAAA CAAATAGCAT CCTTCTTGTT TCATTTACAT 990
 AAGTATTTTC TGTGGGACCG ACTCTCAAGG CACTGTGTAT GCCCTGCAAG TTGGCTGTCT 1050
 ATGAGCATTT AGAGATTTAG AAGAAAAATT TAGTTTGTTT AACCTTGTA ACTGTTTGTT 1110
 TTGTTGTTGT TTTTTTTTCA AGCCAAATAC ATGACATAAG ATCAATAAAG AGGCCAAATT 1170
 TTTAGCTGTT TTATGT 1186

Sequence No.: 63

Sequence length: 1409

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Lymphoma

Cell line: U937

Clone name: HP10136

Sequence characteristics

Code representing characteristics: CDS

Existence site: 82.. 729

Characterization method: E

Sequence description

ATAACTGTTG TCGCGGCGGA GGAAGTGAGG ACGGCGCCAA GGGCCTTCCG GGCCAGTGT	60
GGATCCCTGT AGTTTGTGAA G ATG GTG TTG CTA ACA ATG ATC GCC CGA GTG	111
Met Val Leu Leu Thr Met Ile Ala Arg Val	
1 5 10	
GCG GAC GGG CTC CCG CTG GCC GCC TCG ATG CAG GAG GAC GAA CAG TCT	159
Ala Asp Gly Leu Pro Leu Ala Ala Ser Met Gln Glu Asp Glu Gln Ser	
15 20 25	
GGC CGG GAC CTT CAA CAG TAT CAG AGT CAG GCT AAG CAA CTC TTT CGA	207
Gly Arg Asp Leu Gln Gln Tyr Gln Ser Gln Ala Lys Gln Leu Phe Arg	
30 35 40	
AAG TTG AAT GAA CAG TCC CCT ACC AGA TGT ACC TTG GAA GCA GGA GCC	255
Lys Leu Asn Glu Gln Ser Pro Thr Arg Cys Thr Leu Glu Ala Gly Ala	
45 50 55	
ATG ACT TTT CAC TAC ATT ATT GAG CAG GGG GTG TGT TAT TTG GTT TTA	303
Met Thr Phe His Tyr Ile Ile Glu Gln Gly Val Cys Tyr Leu Val Leu	
60 65 70	
TGT GAA GCT GCC TTC CCT AAG AAG TTG GCT TTT GCC TAC CTA GAA GAT	351
Cys Glu Ala Ala Phe Pro Lys Lys Leu Ala Phe Ala Tyr Leu Glu Asp	
75 80 85 90	
TTG CAC TCA GAA TTT GAT GAA CAG CAT GGA AAG AAG GTG CCC ACT GTG	399
Leu His Ser Glu Phe Asp Glu Gln His Gly Lys Lys Val Pro Thr Val	
95 100 105	
TCC CGA CCC TAT TCC TTT ATT GAA TTT GAT ACT TTC ATT CAG AAA ACC	447
Ser Arg Pro Tyr Ser Phe Ile Glu Phe Asp Thr Phe Ile Gln Lys Thr	
110 115 120	
AAG AAG CTC TAC ATT GAC AGT CGT GCT CGA AGA AAT CTA GGC TCC ATC	495
Lys Lys Leu Tyr Ile Asp Ser Arg Ala Arg Arg Asn Leu Gly Ser Ile	
125 130 135	
AAC ACT GAA TTG CAA GAT GTG CAG AGG ATC ATG GTG GCC AAT ATT GAA	543
Asn Thr Glu Leu Gln Asp Val Gln Arg Ile Met Val Ala Asn Ile Glu	
140 145 150	
GAA GTG TTA CAA CGA GGA GAA GCA CTC TCA GCA TTG GAT TCA AAG GCT	591
Glu Val Leu Gln Arg Gly Glu Ala Leu Ser Ala Leu Asp Ser Lys Ala	
155 160 165 170	

155

AAC AAT TTG TCC AGT CTG TCC AAG AAA TAC CGC CAG GAT GCG AAG TAC 639
 Asn Asn Leu Ser Ser Leu Ser Lys Lys Tyr Arg Gln Asp Ala Lys Tyr
 175 180 185
 TTG AAC ATG CGT TCC ACT TAT GCC AAA CTT GCA GCA GTA GCT GTA TTT 687
 Leu Asn Met Arg Ser Thr Tyr Ala Lys Leu Ala Ala Val Ala Val Phe
 190 195 200
 TTC ATC ATG TTA ATA GTG TAT GTC CGA TTC TGG TGG CTG TGAA 730
 Phe Ile Met Leu Ile Val Tyr Val Arg Phe Trp Trp Leu
 205 210 215
 ATAATGAATA CAGTCACTGG TAAGGGAGAA CCTAGAACCC AGTAGGTGTA TATTTTCAGG 790
 AAAC TGAGCT CACAGAGATG TGTATTAGAA TCCAAGTGGA ACTTCTGCCT CTAAAGACCT 850
 TGCAAGAAAA GAGATGCCCT GAAAATGAAA GGTTCACCT CATTTAATGA AGCTTAACCC 910
 TATGTAGAAA GTCTCTTTTCG GGGGCAGAGG CTTTCTCTGG GTGCCAAGCC ATATATATTA 970
 GGGAAATAGTA GATTGTTAAT TTCGTTTTTTT CCCTCCCAGT GCATTTTAAA AACAGCACTG 1030
 GCTGGGGCAT TCTCATTCTC TGATGGAGCC ATCAATGAGA TTAACTTAG TCAACCTGTG 1090
 CTAGCAACAT TCTGAAATTC CTTCAAAGAA GGCAGTCCTT TGGAAGGTG TTTTTTTTTT 1150
 TTTTTTTTTT TTTGACTCTA ATCAACATTC CTTTGTGTTG TGACATTTGT GATTTTCAGT 1210
 AATCTGAGTT TTTGATGGCC TTTTAAACAA GACTCCAGTA TGTGAAGGTT AATTGCTGTG 1270
 CTCCACAGAT CTTGTCTATT GGCCCCGTGTA GAAAGTTAAC CTTTGTGTTT TCCCTTTTAT 1330
 AATTTGCTTA TTGCACAATT GCTTTAGGGT AAGTGAATTA TATTAAGATG CCTTGAAATT 1390
 ATAGCACTCC TTGATTAAG 1409

Sequence No.: 64

Sequence length: 974

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Stomach cancer

Clone name: HP10175

Sequence characteristics

Code representing characteristics: CDS

Existence site: 174.. 512

Characterization method: E

Sequence description

AGAGCCGCTC CCCTCTCCTC GCCCCGCCAC CGGGACGGAG AGCGCCCGCC GCTGCATTTT 60
 CGGCGACACC TCGCAGTCAT TCCTGCGGCT TCGCGCGCCCT TGTAGACAGC CGGGGCCTTC 120
 GTGAGACCGG TGCAGGCCTG GGGTAGTCTC CTGTCTGGAC AGAGAAGAGA AAA ATG 176
 Met

Year	1950	1951	1952	1953	1954	1955	1956	1957	1958	1959	1960	1961	1962	1963	1964	1965	1966	1967	1968	1969	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1950	1951	1952	1953	1954	1955	1956	1957	1958	1959	1960	1961	1962	1963	1964	1965	1966	1967	1968	1969	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

Sequence No.: 65
Sequence length: 925
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
Organism species: *Homo sapiens*
Cell kind: Epidermoid carcinoma
Cell line: KB
Clone name: HP10179
Sequence characteristics
Code representing characteristics: CDS

157

Existence site: 122.. 466

Characterization method: E

Sequence description

AATCGCGTTT CCGGAGAGAC CTGGCTGCTG TGTCCGCGG CTTGCGCTCC GTAGTGGACT	60
CCGCGGGCCT TCGGCAGATG CAGGCCTGGG GTAGTCTCCT TTCTGGACTG AGAAGAGAAG	120
ATG GAG AAG CCC CTC TTC CCA TTA GTG CCT TTG CAT TGG TTT GGC TTT	168
Met Glu Lys Pro Leu Phe Pro Leu Val Pro Leu His Trp Phe Gly Phe	
1 5 10 15	
GGC TAC ACA GCA CTG GTT GTT TCT GGT GGG ATC GTT GGC TAT GTA AAA	216
Gly Tyr Thr Ala Leu Val Val Ser Gly Gly Ile Val Gly Tyr Val Lys	
20 25 30	
ACA GGC AGC GTG CCG TCC CTG GCA GCA GGG CTG CTC TTC GGC AGT CTA	264
Thr Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Leu	
35 40 45	
GCC GGC CTG GGT GCT TAC CAG CTG TAT CAG GAT CCT AGG AAC GTT TGG	312
Ala Gly Leu Gly Ala Tyr Gln Leu Tyr Gln Asp Pro Arg Asn Val Trp	
50 55 60	
GGT TTC CTA GCC GCT ACA TCT GTT ACT TTT GTT GGT GTT ATG GGA ATA	360
Gly Phe Leu Ala Ala Thr Ser Val Thr Phe Val Gly Val Met Gly Met	
65 70 75 80	
AGA TCC TAC TAC TAT GGA AAA TTC ATG CCT GTA GGT TTA ATT GCA GGT	408
Arg Ser Tyr Tyr Tyr Gly Lys Phe Met Pro Val Gly Leu Ile Ala Gly	
85 90 95	
GCC AGT TTG CTG ATG GCC GCC AAA GTT GGA GTT CGT ATG TTG ATG ACA	456
Ala Ser Leu Leu Met Ala Ala Lys Val Gly Val Arg Met Leu Met Thr	
100 105 110	
TCT GAT TAGCAGAAGT CATGTTGCA GCTTGACTC ATGAAGGATT AAAAAATCT	510
Ser Asp	
GCATCTTCCA CTATTTTCAA TGTATTAAGA GAAATAAGTG CAGCATTTTT GCATCTGACA	570
TTTTACCTAA AAAAAAAAAAG ACACCAAATT TGGCGGAGGG GTGAAAAATC AGTTGTTACC	630
ATTATAACCC TACAGAGGTG GTGAGCATGT AACATGAGCT TATTGAGACC ATCATAGAGA	690
TCGATTCTTG TATATTGATT TTATCTCTTT CTGTATCTAT AGGTAAATCT CAAGGGTAAA	750
ATGTTAGGTG TTGACATTGA GAACCTGAA ACCCCATTCC CTGCTCAGAG GAACAGTGTG	810
AAAAAAATC TCTTGAGAGA TTTAGAATAT CTTTCTTTT GCTCATCTTA GACCACAGAC	870
TGACTTTGAA ATTATGTTAA GTGAAATATC AATGAAAATA AAGTTTACTA TAAAT	925

Sequence No.: 66

Sequence length: 1115

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Fibrosarcoma

Cell line: HT-1080

Clone name: HP10196

Sequence characteristics

Code representing characteristics: CDS

Existence site: 10.. 993

Characterization method: E

Sequence description

```

GCGGGGAAA ATG GCG GCG GCG GCG GCG GCG GCT GCA GCT ACG AAC GGG ACC      51
      Met Ala Ala Ala Ala Ala Ala Ala Ala Ala Thr Asn Gly Thr
              1              5              10
GGA GGA AGC AGC GGG ATG GAG GTG GAT GCA GCA GTA GTC CCC AGC GTG      99
Gly Gly Ser Ser Gly Met Glu Val Asp Ala Ala Val Val Pro Ser Val
      15              20              25              30
ATG GCC TGC GGA GTG ACT GGG AGT GTT TCC GTC GCT CTC CAT CCC CTT      147
Met Ala Cys Gly Val Thr Gly Ser Val Ser Val Ala Leu His Pro Leu
              35              40              45
GTC ATT CTC AAC ATC TCA GAC CAC TGG ATC CGC ATG CGC TCC CAG GAG      195
Val Ile Leu Asn Ile Ser Asp His Trp Ile Arg Met Arg Ser Gln Glu
              50              55              60
GGG CGG CCT GTG CAG GTG ATT GGG GCT CTG ATT GGC AAG CAG GAG GGC      243
Gly Arg Pro Val Gln Val Ile Gly Ala Leu Ile Gly Lys Gln Glu Gly
              65              70              75
CGA AAT ATC GAG GTG ATG AAC TCC TTT GAG CTG CTG TCC CAC ACC GTG      291
Arg Asn Ile Glu Val Met Asn Ser Phe Glu Leu Leu Ser His Thr Val
              80              85              90
GAA GAG AAG ATT ATC ATT GAC AAG GAA TAT TAT TAC ACC AAG GAG GAG      339
Glu Glu Lys Ile Ile Ile Asp Lys Glu Tyr Tyr Tyr Thr Lys Glu Glu
              95              100              105              110
CAG TTT AAA CAG GTG TTC AAG GAG CTG GAG TTT CTG GGT TGG TAT ACC      387
Gln Phe Lys Gln Val Phe Lys Glu Leu Glu Phe Leu Gly Trp Tyr Thr
              115              120              125
ACA GCG GGG CCA CCT GAC CCC TCG GAC ATC CAC GTC CAT AAG CAG GTG      435
Thr Gly Gly Pro Pro Asp Pro Ser Asp Ile His Val His Lys Gln Val
              130              135              140
TGT GAG ATC ATC GAG AGC CCC CTC TTT CTG AAG TTG AAC CCT ATG ACC      483
Cys Glu Ile Ile Glu Ser Pro Leu Phe Leu Lys Leu Asn Pro Met Thr
              145              150              155
AAG CAC ACA GAT CTT CCT GTC AGC GTT TTT GAG TCT GTC ATT GAT ATA      531
Lys His Thr Asp Leu Pro Val Ser Val Phe Glu Ser Val Ile Asp Ile

```

159

160 165 170 579
 ATC AAT GGA GAG GCC ACA ATG CTG TTT GCT GAG CTG ACC TAC ACT CTG
 Ile Asn Gly Glu Ala Thr Met Leu Phe Ala Glu Leu Thr Tyr Thr Leu
 175 180 185 190 627
 GCC ACA GAG GAA GCG GAA CGC ATT GGT GTA GAC CAC GTA GCC CGA ATG
 Ala Thr Glu Glu Ala Glu Arg Ile Gly Val Asp His Val Ala Arg Met
 195 200 205 675
 ACA GCA ACA GGC AGT GGA GAG AAC TCC ACT GTG GCT GAA CAC CTG ATA
 Thr Ala Thr Gly Ser Gly Glu Asn Ser Thr Val Ala Glu His Leu Ile
 210 215 220 723
 GCA CAG CAC AGC GCC ATC AAG ATG CTG CAC AGC CGC GTC AAG CTC ATC
 Ala Gln His Ser Ala Ile Lys Met Leu His Ser Arg Val Lys Leu Ile
 225 230 235 771
 TTG GAG TAC GTC AAG GCC TCT GAA GCG GGA GAG GTC CCC TTT AAT CAT
 Leu Glu Tyr Val Lys Ala Ser Glu Ala Gly Glu Val Pro Phe Asn His
 240 245 250 819
 GAG ATC CTG CGG GAG GCC TAT GCT CTG TGT CAC TGT CTC CCG GTG CTC
 Glu Ile Leu Arg Glu Ala Tyr Ala Leu Cys His Cys Leu Pro Val Leu
 255 260 265 270 867
 AGC ACA GAC AAG TTC AAG ACA GAT TTT TAT GAT CAA TGC AAC GAC GTG
 Ser Thr Asp Lys Phe Lys Thr Asp Phe Tyr Asp Gln Cys Asn Asp Val
 275 280 285 915
 GGG CTC ATG GCC TAC CTC GGC ACC ATC ACC AAA ACG TGC AAC ACC ATG
 Gly Leu Met Ala Tyr Leu Gly Thr Ile Thr Lys Thr Cys Asn Thr Met
 290 295 300 963
 AAC CAG TTT GTG AAC AAG TTC AAT GTC CTC TAC GAC CGA CAA GGC ATC
 Asn Gln Phe Val Asn Lys Phe Asn Val Leu Tyr Asp Arg Gln Gly Ile
 305 310 315 1000
 GGC AGG AGA ATG CGC GGC CTC TTT TTC TGATGAGGGT
 Gly Arg Arg Met Arg Gly Leu Phe Phe
 320 325 1060
 ACTTGAAGGG CTGATGGACA GGGGTCAGGC AACTATCCCA AAGGGGAGGG CACTACACTT
 CCTTGAGAGA AACCACTGTC ATTAATAAAA GGGGAGCAGC CCCTGAGCAC CCCTG 1115

Sequence No.: 67

Sequence length: 1721

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Fibrosarcoma

160

Cell line: HT-1080

Clone name: HP10235

Sequence characteristics

Code representing characteristics: CDS

Existence site: 6.. 1127

Characterization method: E

Sequence description

ATGTC ATG ACC CTA TGT GCC ATG CTG CCC CTG CTG TTA TTC ACC TAC CTC	50
Met Thr Leu Cys Ala Met Leu Pro Leu Leu Leu Phe Thr Tyr Leu	
1 5 10 15	
AAC TCC TTC CTG CAT CAG AGG ATC CCC CAG TCC GTA CGG ATC CTG GGC	98
Asn Ser Phe Leu His Gln Arg Ile Pro Gln Ser Val Arg Ile Leu Gly	
20 25 30	
AGC CTG GTG GCC ATC CTG CTG GTG TTT CTG ATC ACT GCC ATC CTG GTG	146
Ser Leu Val Ala Ile Leu Leu Val Phe Leu Ile Thr Ala Ile Leu Val	
35 40 45	
AAG GTG CAG CTG GAT GCT CTG CCC TTC TTT GTC ATC ACC ATG ATC AAG	194
Lys Val Gln Leu Asp Ala Leu Pro Phe Phe Val Ile Thr Met Ile Lys	
50 55 60	
ATC GTG CTC ATT AAT TCA TTT GGT GCC ATC CTG CAG GGC AGC CTG TTT	242
Ile Val Leu Ile Asn Ser Phe Gly Ala Ile Leu Gln Gly Ser Leu Phe	
65 70 75	
GGT CTG GCT GGC CTT CTG CCT GCC AGC TAC ACG GCC CCC ATC ATG AGT	290
Gly Leu Ala Gly Leu Leu Pro Ala Ser Tyr Thr Ala Pro Ile Met Ser	
80 85 90 95	
GGC CAG GGC CTA GCA GGC TTC TTT GCC TCC GTG GCC ATG ATC TGC GCT	338
Gly Gln Gly Leu Ala Gly Phe Phe Ala Ser Val Ala Met Ile Cys Ala	
100 105 110	
ATT GCC AGT GGC TCG GAG CTA TCA GAA AGT GCC TTC GGC TAC TTT ATC	386
Ile Ala Ser Gly Ser Glu Leu Ser Glu Ser Ala Phe Gly Tyr Phe Ile	
115 120 125	
ACA GCC TGT GCT GTT ATC ATT TTG ACC ATC ATC TGT TAC CTG GGC CTG	434
Thr Ala Cys Ala Val Ile Ile Leu Thr Ile Ile Cys Tyr Leu Gly Leu	
130 135 140	
CCC CGC CTG GAA TTC TAC CGC TAC TAC CAG CAG CTC AAG CTT GAA GGA	482
Pro Arg Leu Glu Phe Tyr Arg Tyr Tyr Gln Gln Leu Lys Leu Glu Gly	
145 150 155	
CCC GGG GAG CAG GAG ACC AAG TTG GAC CTC ATT AGC AAA GGA GAG GAG	530
Pro Gly Glu Gln Glu Thr Lys Leu Asp Leu Ile Ser Lys Gly Glu Glu	
160 165 170 175	
CCA AGA GCA GGC AAA GAG GAA TCT GGA GTT TCA GTC TCC AAC TCT CAG	578
Pro Arg Ala Gly Lys Glu Glu Ser Gly Val Ser Val Ser Asn Ser Gln	
180 185 190	

161

CCC ACC AAT GAA AGC CAC TCT ATC AAA GCC ATC CTG AAA AAT ATC TCA	626
Pro Thr Asn Glu Ser His Ser Ile Lys Ala Ile Leu Lys Asn Ile Ser	
195 200 205	
GTC CTG GCT TTC TCT GTC TGC TTC ATC TTC ACT ATC ACC ATT GGG ATG	674
Val Leu Ala Phe Ser Val Cys Phe Ile Phe Thr Ile Thr Ile Gly Met	
210 215 220	
TTT CCA GCC GTG ACT GTT GAG GTC AAG TCC AGC ATC GCA GGC AGC AGC	722
Phe Pro Ala Val Thr Val Glu Val Lys Ser Ser Ile Ala Gly Ser Ser	
225 230 235	
ACC TGG GAA CGT TAC TTC ATT CCT GTG TCC TGT TTC TTG ACT TTC AAT	770
Thr Trp Glu Arg Tyr Phe Ile Pro Val Ser Cys Phe Leu Thr Phe Asn	
240 245 250 255	
ATC TTT GAC TGG TTG GGC CGG AGC CTC ACA GCT GTA TTC ATG TGG CCT	818
Ile Phe Asp Trp Leu Gly Arg Ser Leu Thr Ala Val Phe Met Trp Pro	
260 265 270	
GGG AAG GAC AGC CGC TGG CTG CCA AGC CTG GTG CTG GCC CGG CTG GTG	866
Gly Lys Asp Ser Arg Trp Leu Pro Ser Leu Val Leu Ala Arg Leu Val	
275 280 285	
TTT GTG CCA CTG CTG CTG CTG TGC AAC ATT AAG CCC CGC CGC TAC CTG	914
Phe Val Pro Leu Leu Leu Leu Cys Asn Ile Lys Pro Arg Arg Tyr Leu	
290 295 300	
ACT GTG GTC TTC GAG CAC GAT GCC TGG TTC ATC TTC TTC ATG GCT GCC	962
Thr Val Val Phe Glu His Asp Ala Trp Phe Ile Phe Phe Met Ala Ala	
305 310 315	
TTT GCC TTC TCC AAC GGC TAC CTC GCC AGC CTC TGC ATG TGC TTC GGG	1010
Phe Ala Phe Ser Asn Gly Tyr Leu Ala Ser Leu Cys Met Cys Phe Gly	
320 325 330 335	
CCC AAG AAA GTG AAG CCA GCT GAG GCA GAG ACC GCA GGA GCC ATC ATG	1058
Pro Lys Lys Val Lys Pro Ala Glu Ala Glu Thr Ala Gly Ala Ile Met	
340 345 350	
GCC TTC TTC CTG TGT CTG GGT CTG GCA CTG GGG GCT GTT TTC TCC TTC	1106
Ala Phe Phe Leu Cys Leu Gly Leu Ala Leu Gly Ala Val Phe Ser Phe	
355 360 365	
CTG TTC CGG GCA ATT GTG TGACAAAGGA TGGACAGAAG GACTGC	1150
Leu Phe Arg Ala Ile Val	
370	
CTGCCTCCCT CCCTGTCTGC CTCCTGCCCC TTCCTTCTGC CAGGGGTGAT CCTGAGTGGT	1210
CTGGCGGTTT TTTCTTCTAA CTGACTTCTG CTTTCCACGG CGTGTGCTGG GCCCGGATCT	1270
CCAGGCCCTG GGGAGGGAGC CTCTGGACGG ACAGTGGGGA CATTGTGGGT TTGGGGCTCA	1330
GAGTCGAGGG ACGGGGTGTA GCCTCGGCAT TTGCTTGAGT TTCTCCACTC TTGGCTCTGA	1390
CTGATCCCTG CTTGTGCAGG CCAGTGGAGG CTCTTGGGCT TGGAGAACAC GTGTGTCTCT	1450
GTGTATGTGT CTGTGTGTCT GCGTCCGTGT CTGTCAGACT GTCTGCCTGT CCTGGGGTGG	1510
CTAGGAGCTG GGTCTGACCG TTGTATGGTT TGACCTGATA TACTCCATTC TCCCCTGCGC	1570
CTCCTCTCT GTGTTCTCTC CATGTCCCC TCCCAACTCC CCATGCCCAG TTCTTACCCA	1630

162

TCATGCACCC TGTACAGTTG CCACGTTACT GCCTTTTTTA AAAATATATT TGACAGAAAC 1690
 CAGGTGCCTT CAGAGGCTCT CTGATTTAAA T 1721

Sequence No.: 68
 Sequence length: 1504
 Sequence type: Nucleic acid
 Strandedness: Double
 Topology: Linear
 Sequence kind: cDNA to mRNA
 Original source:

Organism species: *Homo sapiens*

Cell kind: Stomach cancer

Clone name: HP10297

Sequence characteristics

Code representing characteristics: CDS

Existence site: 63.. 614

Characterization method: E

Sequence description

CTTTTGCGGC TGCAGCGGC TTGTAGGTGT CCGGCTTTC TGGCCAGCA AGCCTGATAA 60
 GC ATG AAG CTC TTA TCT TTG GTG GCT GTG GTC GGG TGT TTG CTG GTG 107
 Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val
 1 5 10 15
 CCC CCA GCT GAA GCC AAC AAG AGT TCT GAA GAT ATC CGG TGC AAA TGC 155
 Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys
 20 25 30
 ATC TGT CCA CCT TAT AGA AAC ATC AGT GGG CAC ATT TAC AAC CAG AAT 203
 Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn
 35 40 45
 GTA TCC CAG AAG GAC TGC AAC TGC CTG CAC GTG GTG GAG CCC ATG CCA 251
 Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro
 50 55 60
 GTG CCT GGC CAT GAC GTG GAG GCC TAC TGC CTG CTG TGC GAG TGC AGG 299
 Val Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg
 65 70 75
 TAC GAG GAG CGC AGC ACC ACC ACC ATC AAG GTC ATC ATT GTC ATC TAC 347
 Tyr Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr
 80 85 90 95
 CTG TCC GTG GTG GGT GCC CTG TTG CTC TAC ATG GCC TTC CTG ATG CTG 395
 Leu Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu
 100 105 110
 GTG GAC CCT CTG ATC CGA AAG CCG GAT GCA TAC ACT GAG CAA CTG CAC 443
 Val Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His

163

115	120	125	491
AAT GAG GAG GAG AAT GAG GAT GCT CGC TCT ATG GCA GCA GCT GCT GCA			
Asn Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ala			
130	135	140	539
TCC CTC GGG GGA CCC CGA GCA AAC ACA GTC CTG GAG CGT GTG GAA GGT			
Ser Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly			
145	150	155	587
GCC CAG CAG CGG TGG AAG CTG CAG GTG CAG GAG CAG CGG AAG ACA GTC			
Ala Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val			
160	165	170	640
TTC GAT CGG CAC AAG ATG CTC AGC TAGATGGGCT GGTGTGGTTG GGTCAAGGC			
Phe Asp Arg His Lys Met Leu Ser			
180			
CCCAACACCA TGGCTGCCAG CTTCCAGGCT GGACAAAGCA GGGGGCTACT TCTCCCTTCC			700
CTCGGTTCCA GTCTTCCCTT TAAAAGCCTG TGGCATTTTT CCTCCTTCTC CCTAACTTTA			760
GAAATGTTGT ACTTGGCTAT TTTGATTAGG GAAGAGGGAT GTGGTCTCTG ATCTCTGTTG			820
TCTTCTTGGG TCTTTGGGGT TGAAGGGAGG GGGAAGGCAG GCCAGAAGGG AATGGAGACA			880
TTCGAGGCGG CCTCAGGAGT GGATGCCATC TGTCTCTCCT GGCTCCACTC TTGCCGCCCTT			940
CCAGCTCTGA GTCTTGGGAA TGTTGTTACC CTTGGAAGAT AAAGCTGGGT CTTCAGGAAC			1000
TCAGTGTCTG GGAGGAAAGC ATGGCCCAGC ATTCAGCATG TGTTCCTTTC TGCAGTGGTT			1060
CTTATCACCA CCTCCCTCCC AGCCCCAGCG CCTCAGCCCC AGCCCCAGCT CCAGCCCTGA			1120
GGACAGCTCT GATGGGAGAG CTGGGCCCCC TGAGCCCACT GGGTCTTCAG GGTGCACTGG			1180
AAGCTGGTGT TCGCTGTCCC CTGTGCACTT CTCGCACTGG GGCATGGAGT GCCCATGCAT			1240
ACTCTGCTGC CGGTCCCCCT ACCTGCACTT GAGGGGTCTG GGCAGTCCCT CCTCTCCCCA			1300
GTGTCCACAG TCACTGAGCC AGACGGTCGG TTGGAACATG AGACTCGAGG CTGAGCGTGG			1360
ATCTGAACAC CACAGCCCCT GTACTTGGGT TGCCTCTTGT CCCTGAACTT CGTTGTACCA			1420
GTGCATGGAG AGAAAATTTT GTCCTCTTGT CTTAGAGTTG TGTGTAAATC AAGGAAGCCA			1480
TCATTAAATT GTTTATTTC TCTC			1504

Sequence No.: 69

Sequence length: 532

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Stomach cancer

Clone name: HP10299

Sequence characteristics

Code representing characteristics: CDS

Existence site: 93.. 443

Characterization method: E

Sequence description

```

GCTCTCTGGT AAAGGCGTGC AGGTGTTGGC CGCGGCCTCT GAGCTGGGAT GAGCCGTGCT      60
CCCCGGTGGAA GCAAGGGAGC CCAGCCGGAG CC ATG GCC AGT ACA GTG GTA GCA      113
                               Met Ala Ser Thr Val Val Ala
                               1           5
GTT GGA CTG ACC ATT GCT GCT GCA GGA TTT GCA GGC CGT TAC GTT TTG      161
Val Gly Leu Thr Ile Ala Ala Ala Gly Phe Ala Gly Arg Tyr Val Leu
      10           15           20
CAA GCC ATG AAG CAT ATG GAG CCT CAA GTA AAA CAA GTT TTT CAA AGC      209
Gln Ala Met Lys His Met Glu Pro Gln Val Lys Gln Val Phe Gln Ser
      25           30           35
CTA CCA AAA TCT GCC TTC AGT GGT GGC TAT TAT AGA GGT GGG TTT GAA      257
Leu Pro Lys Ser Ala Phe Ser Gly Gly Tyr Tyr Arg Gly Gly Phe Glu
      40           45           50           55
CCC AAA ATG ACA AAA CGG GAA GCA GCA TTA ATA CTA GGT GTA AGC CCT      305
Pro Lys Met Thr Lys Arg Glu Ala Ala Leu Ile Leu Gly Val Ser Pro
      60           65           70
ACT GCC AAT AAA GGG AAA ATA AGA GAT GCT CAT CGA CGA ATT ATG CTT      353
Thr Ala Asn Lys Gly Lys Ile Arg Asp Ala His Arg Arg Ile Met Leu
      75           80           85
TTA AAT CAT CCT GAC AAA GGA GGA TCT CCT TAT ATA GCA GCC AAA ATC      401
Leu Asn His Pro Asp Lys Gly Gly Ser Pro Tyr Ile Ala Ala Lys Ile
      90           95           100
AAT GAA GCT AAA GAT TTA CTA GAA GGT CAA GCT AAA AAA TGAAGTAAAT      450
Asn Glu Ala Lys Asp Leu Leu Glu Gly Gln Ala Lys Lys
      105           110           115
GTATGATGAA TTTTAAGTTC GTATTAGTTT ATGTATATGA GTACTAAGTT TTTATAATAA      510
AATGCCTCAG AGCTACAATT TT      532

```

Sequence No.: 70

Sequence length: 662

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Epidermoid carcinoma

Cell line: KB

Clone name: HP10301

Sequence characteristics

165

Code representing characteristics: CDS

Existence site: 92.. 550

Characterization method: E

Sequence description

TCTAGCCCCG CCCCAGGCGA GGGCGCCGCA CCCACACCGC GCTGCGCAGT TTTGTTCTGC 60
 TCCAGCTGTT CGAAGGTGAT CCAGACGCAA G ATG GCT GTC CTC TCT AAG GAA 112
 Met Ala Val Leu Ser Lys Glu
 1 5
 TAT GGT TTT GTG CTT CTA ACT GGT GCT GCC AGC TTT ATA ATG GTG GCC 160
 Tyr Gly Phe Val Leu Leu Thr Gly Ala Ala Ser Phe Ile Met Val Ala
 10 15 20
 CAC CTA GCC ATC AAT GTT TCC AAG GCC CGC AAG AAG TAC AAA GTG GAG 208
 His Leu Ala Ile Asn Val Ser Lys Ala Arg Lys Lys Tyr Lys Val Glu
 25 30 35
 TAT CCT ATC ATG TAC AGC ACG GAC CCT GAA AAT GGG CAC ATC TTC AAC 256
 Tyr Pro Ile Met Tyr Ser Thr Asp Pro Glu Asn Gly His Ile Phe Asn
 40 45 50 55
 TGC ATT CAG CGA GCC CAC CAG AAC ACG TTG GAA GTG TAT CCT CCC TTC 304
 Cys Ile Gln Arg Ala His Gln Asn Thr Leu Glu Val Tyr Pro Pro Phe
 60 65 70
 TTA TTT TTT CTA GCT GTT GGA GGT GTT TAC CAC CCG CGT ATA GCT TCT 352
 Leu Phe Phe Leu Ala Val Gly Gly Val Tyr His Pro Arg Ile Ala Ser
 75 80 85
 GGC CTG GGC TTG GCC TGG ATT GTT GGA CGA GTT CTT TAT GCT TAT GGC 400
 Gly Leu Gly Leu Ala Trp Ile Val Gly Arg Val Leu Tyr Ala Tyr Gly
 90 95 100
 TAT TAC ACG GGA GAA CCC AGC AAG CGT AGT CGA GGA GCC CTG GGC TCC 448
 Tyr Tyr Thr Gly Glu Pro Ser Lys Arg Ser Arg Gly Ala Leu Gly Ser
 105 110 115
 ATC GCC CTC CTG GGC TTG GTG GGC ACA ACT GTG TGC TCT GCT TTC CAG 496
 Ile Ala Leu Leu Gly Leu Val Gly Thr Thr Val Cys Ser Ala Phe Gln
 120 125 130 135
 CAT CTT GGT TGG GTT AAA AGT GGC TTG GGC AGT GGA CCC AAA TGC TGC 544
 His Leu Gly Trp Val Lys Ser Gly Leu Gly Ser Gly Pro Lys Cys Cys
 140 145 150
 CAT TAAAGAATTA TAGGGGTTTA AAAACTCTCA TTCATTTTAA ATG 590
 His
 ACTTACCTTT ATTTCCAGTT ACATTTTTTT TCTAAATATA ATAAAACTT ACCTGGCATC 650
 AGCCTCATAC CT 662

Sequence No.: 71

Sequence length: 2373
 Sequence type: Nucleic acid
 Strandedness: Double
 Topology: Linear
 Sequence kind: cDNA to mRNA
 Original source:

Organism species: *Homo sapiens*

Cell kind: Liver

Clone name: HP10302

Sequence characteristics

Code representing characteristics: CDS

Existence site: 134.. 1813

Characterization method: E

Sequence description

GAAGACCCCA GCGCCGGCGC GGCTCAGGGC TGGGCCACG GGA	CGCTCCGGA CGCGCCGCGA	60
AAGCGTTGCG CTCCCGGAGG CGTCCGCAGC TGCTGGCTGC TCATTG	CCCG GTGACCGGAG	120
GCTCGGGGCC AGC ATG GCC CCC ACG CTG CAA CAG GCG TAC	CGG AGG CGC	169
Met Ala Pro Thr Leu Gln Gln Ala Tyr Arg Arg Arg		
1 5 10		
TGG TGG ATG GCC TGC ACG GCT GTG CTG GAG AAC CTC TTC	TCT GCT	217
Trp Trp Met Ala Cys Thr Ala Val Leu Glu Asn Leu Phe Phe	Ser Ala	
15 20 25		
GTA CTC CTG GGC TGG GGC TCC CTG TTG ATC ATT CTG AAG	AAC GAG GGC	265
Val Leu Leu Gly Trp Gly Ser Leu Leu Ile Ile Leu Lys Asn	Glu Gly	
30 35 40		
TTC TAT TCC AGC ACG TGC CCA GCT GAG AGC AGC ACC AAC	ACC ACC CAG	313
Phe Tyr Ser Ser Thr Cys Pro Ala Glu Ser Ser Thr Asn	Thr Thr Gln	
45 50 55 60		
GAT GAG CAG CGC AGG TGG CCA GGC TGT GAC CAG CAG GAC	GAG ATG CTC	361
Asp Glu Gln Arg Arg Trp Pro Gly Cys Asp Gln Gln Asp	Glu Met Leu	
65 70 75		
AAC CTG GGC TTC ACC ATT GGT TCC TTC GTG CTC AGC GCC	ACC ACC CTG	409
Asn Leu Gly Phe Thr Ile Gly Ser Phe Val Leu Ser Ala	Thr Thr Leu	
80 85 90		
CCA CTG GGG ATC CTC ATG GAC CGC TTT GGC CCC CGA CCC	GTG CGG CTG	457
Pro Leu Gly Ile Leu Met Asp Arg Phe Gly Pro Arg Pro	Val Arg Leu	
95 100 105		
GTT GGC AGT GCC TGC TTC ACT GCG TCC TGC ACC CTC	ATG GCC CTG GCC	505
Val Gly Ser Ala Cys Phe Thr Ala Ser Cys Thr Leu Met	Ala Leu Ala	
110 115 120		
TCC CGG GAC GTG GAA GCT CTG TCT CCG TTG ATA TTC	CTG GCG CTG TCC	553
Ser Arg Asp Val Glu Ala Leu Ser Pro Leu Ile Phe Leu	Ala Leu Ser	
125 130 135 140		

167

CTG AAT GGC TTT GGT GGC ATC TGC CTA ACG TTC ACT TCA CTC ACG CTG 601
 Leu Asn Gly Phe Gly Gly Ile Cys Leu Thr Phe Thr Ser Leu Thr Leu
 145 150 155
 CCC AAC ATG TTT GGG AAC CTG CGC TCC ACG TTA ATG GCC CTC ATG ATT 649
 Pro Asn Met Phe Gly Asn Leu Arg Ser Thr Leu Met Ala Leu Met Ile
 160 165 170
 GGC TCT TAC GCC TCT TCT GCC ATT ACG TTC CCA GGA ATC AAG CTG ATC 697
 Gly Ser Tyr Ala Ser Ser Ala Ile Thr Phe Pro Gly Ile Lys Leu Ile
 175 180 185
 TAC GAT GCC GGT GTG GCC TTC GTG GTC ATC ATG TTC ACC TGG TCT GGC 745
 Tyr Asp Ala Gly Val Ala Phe Val Val Ile Met Phe Thr Trp Ser Gly
 190 195 200
 CTG GCC TGC CTT ATC TTT CTG AAC TGC ACC CTC AAC TGG CCC ATC GAA 793
 Leu Ala Cys Leu Ile Phe Leu Asn Cys Thr Leu Asn Trp Pro Ile Glu
 205 210 215 220
 GCC TTT CCT GCC CCT GAG GAA GTC AAT TAC ACG AAG AAG ATC AAG CTG 841
 Ala Phe Pro Ala Pro Glu Glu Val Asn Tyr Thr Lys Lys Ile Lys Leu
 225 230 235
 AGT GGG CTG GCC CTG GAC CAC AAG GTG ACA GGT GAC CTC TTC TAC ACC 889
 Ser Gly Leu Ala Leu Asp His Lys Val Thr Gly Asp Leu Phe Tyr Thr
 240 245 250
 CAT GTG ACC ACC ATG GGC CAG AGG CTC AGC CAG AAG GCC CCC AGC CTG 937
 His Val Thr Thr Met Gly Gln Arg Leu Ser Gln Lys Ala Pro Ser Leu
 255 260 265
 GAG GAC GGT TCG GAT GCC TTC ATG TCA CCC CAG GAT GTT CGG GGC ACC 985
 Glu Asp Gly Ser Asp Ala Phe Met Ser Pro Gln Asp Val Arg Gly Thr
 270 275 280
 TCA GAA AAC CTT CCT GAG AGG TCT GTC CCC TTA CGC AAG AGC CTC TGC 1033
 Ser Glu Asn Leu Pro Glu Arg Ser Val Pro Leu Arg Lys Ser Leu Cys
 285 290 295 300
 TCC CCC ACT TTC CTG TGG AGC CTC CTC ACC ATG GGC ATG ACC CAG CTG 1081
 Ser Pro Thr Phe Leu Trp Ser Leu Leu Thr Met Gly Met Thr Gln Leu
 305 310 315
 CGG ATC ATC TTC TAC ATG GCT GCT GTG AAC AAG ATG CTG GAG TAC CTT 1129
 Arg Ile Ile Phe Tyr Met Ala Ala Val Asn Lys Met Leu Glu Tyr Leu
 320 325 330
 GTG ACT GGT GGC CAG GAG CAT GAG ACA AAT GAA CAG CAA CAA AAG GTG 1177
 Val Thr Gly Gly Gln Glu His Glu Thr Asn Glu Gln Gln Gln Lys Val
 335 340 345
 GCA GAG ACA GTT GGG TTC TAC TCC TCC GTC TTC GGG GCC ATG CAG CTG 1225
 Ala Glu Thr Val Gly Phe Tyr Ser Ser Val Phe Gly Ala Met Gln Leu
 350 355 360
 TTG TGC CTT CTC ACC TGC CCC CTC ATT GGC TAC ATC ATG GAC TGG CGG 1273
 Leu Cys Leu Leu Thr Cys Pro Leu Ile Gly Tyr Ile Met Asp Trp Arg

168

365 370 375 380
 ATC AAG GAC TGC GTG GAC GCC CCA ACT CAG GGC ACT GTC CTC GGA GAT 1321
 Ile Lys Asp Cys Val Asp Ala Pro Thr Gln Gly Thr Val Leu Gly Asp
 385 390 395
 GCC AGG GAC GGG GTT GCT ACC AAA TCC ATC AGA CCA CGC TAC TGC AAG 1369
 Ala Arg Asp Gly Val Ala Thr Lys Ser Ile Arg Pro Arg Tyr Cys Lys
 400 405 410
 ATC CAA AAG CTC ACC AAT GCC ATC AGT GCC TTC ACC CTG ACC AAC CTG 1417
 Ile Gln Lys Leu Thr Asn Ala Ile Ser Ala Phe Thr Leu Thr Asn Leu
 415 420 425
 CTG CTT GTG GGT TTT GGC ATC ACC TGT CTC ATC AAC AAC TTA CAC CTC 1465
 Leu Leu Val Gly Phe Gly Ile Thr Cys Leu Ile Asn Asn Leu His Leu
 430 435 440
 CAG TTT GTG ACC TTT GTC CTG CAC ACC ATT GTT CGA GGT TTC TTC CAC 1513
 Gln Phe Val Thr Phe Val Leu His Thr Ile Val Arg Gly Phe Phe His
 445 450 455 460
 TCA GCC TGT GGG AGT CTC TAT GCT GCA GTG TTC CCA TCC AAC CAC TTT 1561
 Ser Ala Cys Gly Ser Leu Tyr Ala Ala Val Phe Pro Ser Asn His Phe
 465 470 475
 GGG ACG CTG ACA GGC CTG CAG TCC CTC ATC AGT GCT GTG TTC GCC TTG 1609
 Gly Thr Leu Thr Gly Leu Gln Ser Leu Ile Ser Ala Val Phe Ala Leu
 480 485 490
 CTT CAG CAG CCA CTT TTC ATG GCG ATG GTG GGA CCC CTG AAA GGA GAG 1657
 Leu Gln Gln Pro Leu Phe Met Ala Met Val Gly Pro Leu Lys Gly Glu
 495 500 505
 CCC TTC TGG GTG AAT CTG GGC CTC CTG CTA TTC TCA CTC CTG GGA TTC 1705
 Pro Phe Trp Val Asn Leu Gly Leu Leu Leu Phe Ser Leu Leu Gly Phe
 510 515 520
 CTG TTG CCT TCC TAC CTC TTC TAT TAC CGT GCC CGG CTC CAG CAG GAG 1753
 Leu Leu Pro Ser Tyr Leu Phe Tyr Tyr Arg Ala Arg Leu Gln Gln Glu
 525 530 535 540
 TAC GCC GCC AAT GGG ATG GGC CCA CTG AAG GTG CTT AGC GGC TCT GAG 1801
 Tyr Ala Ala Asn Gly Met Gly Pro Leu Lys Val Leu Ser Gly Ser Glu
 545 550 555
 GTG ACC GCA TAGACTTCTC AGACCAAGGG ACCTGGATGA 1840
 Val Thr Ala

 CAGGCAATCA AGGCCTGAGC AACC AAAAGG AGTGCCCAT ATGGCTTTTC TACCTGTAAC 1900
 ATGCACATAG AGCCATGGCC GTAGATTTAT AAATACCAAG AGAAGTTCTA TTTTGTAAA 1960
 GACTGCAAAA AGGAGGAAAA AAAAACCTTC AAAAACGCCC CCTAAGTCAA CGCTCCATTG 2020
 ACTGAAGACA GTCCCTATCC TAGAGGGGTT GAGCCTTCTT CCTCCTTGGG TTGAGGAGA 2080
 CCAGGGTGCC TCTTATCTCC TTCTAGCGGT CTGCCTCTG GTACCTCTG GGGGGATCGG 2140
 CAAACAGGCT ACCCCTGAGG TCCCATGTGC CATGAGTGTG CACACATGCA TGTGTCTGTG 2200
 TATGTGTGAA TGTGAGAGAG ACACAGCCCT CCTTTCAGAA GGAAAGGGGC CTGAGGTGCC 2260

AGCTGTGTCC TGGGTTAGGG GTTGGGGGTC GGCCCCCTCC AGGGCCAGGA GGGCAGGTTC 2320
 CCTCTCTGGT GCTGCTGCTT GCAAGTCTTA GAGGAAATAA AAAGGGAAGT GAG 2373

Sequence No.: 72

Sequence length: 1316

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Osteosarcoma

Cell line: U-2 OS

Clone name: HP10304

Sequence characteristics

Code representing characteristics: CDS

Existence site: 11.. 1003

Characterization method: E

Sequence description

GTGTGTTCCAAG ATG GAG GGC GCT CCA CCG GGG TCG CTC GCC CTC CGG CTC 49
 Met Glu Gly Ala Pro Pro Gly Ser Leu Ala Leu Arg Leu
 1 5 10
 CTG CTG TTC GTG GCG CTA CCC GCC TCC GGC TGG CTG ACG ACG GGC GCC 97
 Leu Leu Phe Val Ala Leu Pro Ala Ser Gly Trp Leu Thr Thr Gly Ala
 15 20 25
 CCC GAG CCG CCG CCG CTG TCC GGA GCC CCA CAG GAC GGC ATC AGA ATT 145
 Pro Glu Pro Pro Pro Leu Ser Gly Ala Pro Gln Asp Gly Ile Arg Ile
 30 35 40 45
 AAT GTA ACT ACA CTG AAA GAT GAT GGG GAC ATA TCT AAA CAG CAG GTT 193
 Asn Val Thr Thr Leu Lys Asp Asp Gly Asp Ile Ser Lys Gln Gln Val
 50 55 60
 GTT CTT AAC ATA ACC TAT GAG AGT GGA CAG GTG TAT GTA AAT GAC TTA 241
 Val Leu Asn Ile Thr Tyr Glu Ser Gly Gln Val Tyr Val Asn Asp Leu
 65 70 75
 CCT GTA AAT AGT GGT GTA ACC CGA ATA AGC TGT CAG ACT TTG ATA GTG 289
 Pro Val Asn Ser Gly Val Thr Arg Ile Ser Cys Gln Thr Leu Ile Val
 80 85 90
 AAG AAT GAA AAT CTT GAA AAT TTG GAG GAA AAA GAA TAT TTT GGA ATT 337
 Lys Asn Glu Asn Leu Glu Asn Leu Glu Glu Lys Glu Tyr Phe Gly Ile
 95 100 105
 GTC AGT GTA AGG ATT TTA GTT CAT GAG TGG CCT ATG ACA TCT GGT TCC 385
 Val Ser Val Arg Ile Leu Val His Glu Trp Pro Met Thr Ser Gly Ser

170

110	115	120	125	
AGT TTG CAA CTA ATT GTC ATT CAA GAA GAG GTA GTA GAG ATT GAT GGA				433
Ser Leu Gln Leu Ile Val Ile Gln Glu Glu Val Val Glu Ile Asp Gly				
	130	135	140	
AAA CAA GTT CAG CAA AAG GAT GTC ACT GAA ATT GAT ATT TTA GTT AAG				481
Lys Gln Val Gln Gln Lys Asp Val Thr Glu Ile Asp Ile Leu Val Lys				
	145	150	155	
AAC CGG GGA GTA CTC AGA CAT TCA AAC TAT ACC CTC CCT TTG GAA GAA				529
Asn Arg Gly Val Leu Arg His Ser Asn Tyr Thr Leu Pro Leu Glu Glu				
	160	165	170	
AGC ATG CTC TAC TCT ATT TCT CGA GAC AGT GAC ATT TTA TTT ACC CTT				577
Ser Met Leu Tyr Ser Ile Ser Arg Asp Ser Asp Ile Leu Phe Thr Leu				
	175	180	185	
CCT AAC CTC TCC AAA AAA GAA AGT GTT AGT TCA CTG CAA ACC ACT AGC				625
Pro Asn Leu Ser Lys Lys Glu Ser Val Ser Ser Leu Gln Thr Thr Ser				
	190	195	200	205
CAG TAT CTT ATC AGG AAT GTG GAA ACC ACT GTA GAT GAA GAT GTT TTA				673
Gln Tyr Leu Ile Arg Asn Val Glu Thr Thr Val Asp Glu Asp Val Leu				
	210	215	220	
CCT GGC AAG TTA CCT GAA ACT CCT CTC AGA GCA GAG CCG CCA TCT TCA				721
Pro Gly Lys Leu Pro Glu Thr Pro Leu Arg Ala Glu Pro Pro Ser Ser				
	225	230	235	
TAT AAG GTA ATG TGT CAG TGG ATG GAA AAG TTT AGA AAA GAT CTG TGT				769
Tyr Lys Val Met Cys Gln Trp Met Glu Lys Phe Arg Lys Asp Leu Cys				
	240	245	250	
AGG TTC TGG AGC AAC GTT TTC CCA GTA TTC TTT CAG TTT TTG AAC ATC				817
Arg Phe Trp Ser Asn Val Phe Pro Val Phe Phe Gln Phe Leu Asn Ile				
	255	260	265	
ATG GTG GTT GGA ATT ACA GGA GCA GCT GTG GTA ATA ACC ATC TTA AAG				865
Met Val Val Gly Ile Thr Gly Ala Ala Val Val Ile Thr Ile Leu Lys				
	270	275	280	285
GTG TTT TTC CCA GTT TCT GAA TAC AAA GGA ATT CTT CAG TTG GAT AAA				913
Val Phe Phe Pro Val Ser Glu Tyr Lys Gly Ile Leu Gln Leu Asp Lys				
	290	295	300	
GTG GAC GTC ATA CCT GTG ACA GCT ATC AAC TTA TAT CCA GAT GGT CCA				961
Val Asp Val Ile Pro Val Thr Ala Ile Asn Leu Tyr Pro Asp Gly Pro				
	305	310	315	
GAG AAA AGA GCT GAA AAC CTT GAA GAT AAA ACA TGT ATT TAAACGCCA				1010
Glu Lys Arg Ala Glu Asn Leu Glu Asp Lys Thr Cys Ile				
	320	325	330	
TCTCATATCA TGGACTCCGA AGTAGCCTGT TGCCTCCAAA TTTGCCACTT GAATATAATT				1070
TTCTTTAAAT CGTTAAGAAT CAGTTTATAC ACTAGAGAAA TTGCTAAACT CTAAGACTGC				1130
CTGAAAATTG ACCTTTACAG TGCCAAGTTA AAGTTTACCT TATTCTCGGC CGGGTGCAGT				1190
GGCTCATGCC TGTAATCCCA GGACTTTGGG AGGCCAATGC GGGCGGATCA CGAGGTCAGA				1250

171

TCAAGACCAT CCTGCCAACA TGGTGAAACC CTGTCTCTAC TAAAAAAAAT AAAAAAGTTA 1310
GCTGGG 1316

Sequence No.: 73
Sequence length: 893
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:

Organism species: *Homo sapiens*

Cell kind: Osteosarcoma

Cell line: U-2 OS

Clone name: HP10305

Sequence characteristics

Code representing characteristics: CDS

Existence site: 110.. 436

Characterization method: E

Sequence description

ATCGCGGAGT CGGTGCTTTA GTACGCCGCT GGCACCTTTA CTCTGCCCGG CCGCGCGAAC 60
CCGTTTGAGC TCGGTATCCT AGTGCACAGC CCTTGCAAGC GACGGCGCC ATG AGT CTG 118
Met Ser Leu

1
ACT TCC AGT TCC AGC GTA CGA GTT GAA TGG ATC GCA GCA GTT ACC ATT 166
Thr Ser Ser Ser Ser Val Arg Val Glu Trp Ile Ala Ala Val Thr Ile
5 10 15
GCT GCT GGG ACA GCT GCA ATT GGT TAT CTA GCT TAC AAA AGA TTT TAT 214
Ala Ala Gly Thr Ala Ala Ile Gly Tyr Leu Ala Tyr Lys Arg Phe Tyr
20 25 30 35
GTT AAA GAT CAT CGA AAT AAA GCT ATG ATA AAC CTT CAC ATC CAG AAA 262
Val Lys Asp His Arg Asn Lys Ala Met Ile Asn Leu His Ile Gln Lys
40 45 50
GAC AAC CCC AAG ATA GTA CAT GCT TTT GAC ATG GAG GAT TTG GGA GAT 310
Asp Asn Pro Lys Ile Val His Ala Phe Asp Met Glu Asp Leu Gly Asp
55 60 65
AAA GCT GTG TAC TGC CGT TGT TGG AGG TCC AAA AAG TTC CCA TTC TGT 358
Lys Ala Val Tyr Cys Arg Cys Trp Arg Ser Lys Lys Phe Pro Phe Cys
70 75 80
GAT GGG GCT CAC ACA AAA CAT AAC GAA GAG ACT GGA GAC AAT GTG GGC 406
Asp Gly Ala His Thr Lys His Asn Glu Glu Thr Gly Asp Asn Val Gly
85 90 95
CCT CTG ATC ATC AAG AAA AAA GAA ACT TAAATGGACA CTTTGA 450

[illegible]

TAACAGCGCA	TGCGTGCAGT	GTTGCCTCGC	CCAAAGAAGA	CTACAATCTC	CAGGGAAACC	60
TGGGGCGTCT	CGCGCAAACG	TCCATAACTG	AAAGTAGCTA	AGGCACCCCA	GCCGGAGGAA	120
GTGAGCTCTC	CTGGGGCGTG	GTTGTTCGTG	ATCCTTG CAT	CTGTTACTTA	GGGTCAAGGC	180
TTGGGTCTTG	CCCCGCAGAC	CCTTGGGACG	ACCCGGCCCC	AGCGCAGCT	ATG AAC CTG	238
				Met Asn Leu		

20 25 30 382
TGG TTC TTC CGA GAG GCC TTC CTT GTC CCA GCC TAC ACA GAA CAG AGC
Trp Phe Phe Arg Glu Ala Phe Leu Val Pro Ala Tyr Thr Glu Gln Ser
45 50

173

CAA ATC AAA GGC TAT GTC TGG CGC TCA GCT GTG GGC TTC CTC TTC TGG 430
 Gln Ile Lys Gly Tyr Val Trp Arg Ser Ala Val Gly Phe Leu Phe Trp
 55 60 65
 GTG ATA GTG CTC ACC TCC TGG ATC ACC ATC TTC CAG ATC TAC CGG CCC 478
 Val Ile Val Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile Tyr Arg Pro
 70 75 80
 CGC TGG GGT GCC CTT GGG GAC TAC CTC TCC TTC ACC ATA CCC CTG GGC 526
 Arg Trp Gly Ala Leu Gly Asp Tyr Leu Ser Phe Thr Ile Pro Leu Gly
 85 90 95
 ACC CCC TGACAACTTC TGCACATACT GGGGCCCTGC TTATTCTCCC AGGACAGG 580
 Thr Pro
 100
 CTCCTTAAAG CAGAGGAGCC TGTCTTGGGA GCCCCTTCTC AAACCTCCTAA GACTTGTTTT 640
 CATGTCCCAC GTTCTCTGCT GACATCCCCC AATAAAGGAC CCTAACTTTC 690

Sequence No.: 75

Sequence length: 2186

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Epidermoid carcinoma

Cell line: KB

Clone name: HP10328

Sequence characteristics

Code representing characteristics: CDS

Existence site: 118.. 1236

Characterization method: E

Sequence description

ACTCTTTCTT CGGCTCGCGA GCTGAGAGGA GCAGGTAGAG GGGCAGAGGC GGGACTGTCC 60
 TCTGGGGGAG CCGCCCAGGA GGCTCCTCAG GCCGACCCCA GACCCTGGCT GGCCAGG 117
 ATG AAG TAT CTC CGG CAC CGG CGG CCC AAT GCC ACC CTC ATT CTG GCC 165
 Met Lys Tyr Leu Arg His Arg Arg Pro Asn Ala Thr Leu Ile Leu Ala
 1 5 10 15
 ATC GGC GCT TTC ACC CTC CTC CTC TTC AGT CTG CTA GTG TCA CCA CCC 213
 Ile Gly Ala Phe Thr Leu Leu Leu Phe Ser Leu Leu Val Ser Pro Pro
 20 25 30
 ACC TGC AAG GTC CAG GAG CAG CCA CCG GCG ATC CCC GAG GCC CTG GCC 261
 Thr Cys Lys Val Gln Glu Gln Pro Pro Ala Ile Pro Glu Ala Leu Ala
 35 40 45

174

TGG CCC ACT CCA CCC ACC CGC CCA GCC CCG GCC CCG TGC CAT GCC AAC	309
Trp Pro Thr Pro Pro Thr Arg Pro Ala Pro Ala Pro Cys His Ala Asn	
50 55 60	
ACC TCT ATG GTC ACC CAC CCG GAC TTC GCC ACG CAG CCG CAG CAC GTT	357
Thr Ser Met Val Thr His Pro Asp Phe Ala Thr Gln Pro Gln His Val	
65 70 75 80	
CAG AAC TTC CTC CTG TAC AGA CAC TGC CGC CAC TTT CCC CTG CTG CAG	405
Gln Asn Phe Leu Leu Tyr Arg His Cys Arg His Phe Pro Leu Leu Gln	
85 90 95	
GAC GTG CCC CCC TCT AAG TGC GCG CAG CCG GTC TTC CTG CTG CTG GTG	453
Asp Val Pro Pro Ser Lys Cys Ala Gln Pro Val Phe Leu Leu Leu Val	
100 105 110	
ATC AAG TCC TCC CCT AGC AAC TAT GTG CGC CGC GAG CTG CTG CGG CGC	501
Ile Lys Ser Ser Pro Ser Asn Tyr Val Arg Arg Glu Leu Leu Arg Arg	
115 120 125	
ACG TGG GGC CGC GAG CGC AAG GTA CCG GGT TTG CAG CTG CGC CTC CTC	549
Thr Trp Gly Arg Glu Arg Lys Val Arg Gly Leu Gln Leu Arg Leu Leu	
130 135 140	
TTC CTG GTG GGC ACA GCC TCC AAC CCG CAC GAG GCC CGC AAG GTC AAC	597
Phe Leu Val Gly Thr Ala Ser Asn Pro His Glu Ala Arg Lys Val Asn	
145 150 155 160	
CGG CTG CTG GAG CTG GAG GCA CAG ACT CAC GGA GAC ATC CTG CAG TGG	645
Arg Leu Leu Glu Leu Glu Ala Gln Thr His Gly Asp Ile Leu Gln Trp	
165 170 175	
GAC TTC CAC GAC TCC TTC TTC AAC CTC ACG CTC AAG CAG GTC CTG TTC	693
Asp Phe His Asp Ser Phe Phe Asn Leu Thr Leu Lys Gln Val Leu Phe	
180 185 190	
TTA CAG TGG CAG GAG ACA AGG TGC GCC AAC GCC AGC TTC GTG CTC AAC	741
Leu Gln Trp Gln Glu Thr Arg Cys Ala Asn Ala Ser Phe Val Leu Asn	
195 200 205	
GGG GAT GAT GAC GTC TTT GCA CAC ACA GAC AAC ATG GTC TTC TAC CTG	789
Gly Asp Asp Asp Val Phe Ala His Thr Asp Asn Met Val Phe Tyr Leu	
210 215 220	
CAG GAC CAT GAC CCT GGC CGC CAC CTC TTC GTG GGG CAA CTG ATC CAA	837
Gln Asp His Asp Pro Gly Arg His Leu Phe Val Gly Gln Leu Ile Gln	
225 230 235 240	
AAC GTG GGC CCC ATC CGG GCT TTT TGG AGC AAG TAC TAT GTG CCA GAG	885
Asn Val Gly Pro Ile Arg Ala Phe Trp Ser Lys Tyr Tyr Val Pro Glu	
245 250 255	
GTG GTG ACT CAG AAT GAG CGG TAC CCA CCC TAT TGT GGG GGT GGT GGC	933
Val Val Thr Gln Asn Glu Arg Tyr Pro Pro Tyr Cys Gly Gly Gly Gly	
260 265 270	
TTC TTG CTG TCC CGC TTC ACG GCC GCT GCC CTG CGC CGT GCT GCC CAT	981
Phe Leu Leu Ser Arg Phe Thr Ala Ala Ala Leu Arg Arg Ala Ala His	

175

275	280	285	
GTC TTG GAC ATC TTC CCC ATT GAT GAT GTC TTC CTG GGT ATG TGT CTG			1029
Val Leu Asp Ile Phe Pro Ile Asp Asp Val Phe Leu Gly Met Cys Leu			
290	295	300	
GAG CTT GAG GGA CTG AAG CCT GCC TCC CAC AGC GGC ATC CGC ACG TCT			1077
Glu Leu Glu Gly Leu Lys Pro Ala Ser His Ser Gly Ile Arg Thr Ser			
305	310	315	320
GGC GTG CGG GCT CCA TCG CAA CAC CTG TCC TCC TTT GAC CCC TGC TTC			1125
Gly Val Arg Ala Pro Ser Gln His Leu Ser Ser Phe Asp Pro Cys Phe			
325	330	335	
TAC CGA GAC CTG CTG CTG GTG CAC CGC TTC CTA CCT TAT GAG ATG CTG			1173
Tyr Arg Asp Leu Leu Leu Val His Arg Phe Leu Pro Tyr Glu Met Leu			
340	345	350	
CTC ATG TGG GAT GCG CTG AAC CAG CCC AAC CTC ACC TGC GGC AAT CAG			1221
Leu Met Trp Asp Ala Leu Asn Gln Pro Asn Leu Thr Cys Gly Asn Gln			
355	360	365	
ACA CAG ATC TAC TGAGTCAGCA TCAGGGTCCC CAGCCTCTGG GCTCCTG			1270
Thr Gln Ile Tyr			
370			
TTTCCATAGG AAGGGGCGAC ACCTTCCTCC CAGGAAGCTG AGACCTTTGT GGTCTGAGCA			1330
TAAGGGAGTG CCAGGGAAGG TTTGAGGTTT GATGAGTGAA TATTCTGGCT GGCGAACTCC			1390
TACACATCCT TCAAAAACCCA CCTGGTACTG TTCCAGCATC TTCCCTGGAT GGCTGGAGGA			1450
ACTCCAGAAA ATATCCATCT TCTTTTTGTG GCTGCTAATG GCAGAAGTGC CTGTGCTAGA			1510
GTTCCAACTG TGGATGCATC CGTCCCCTTT GAGTCAAAGT CTTACTTCCC TGCTCTCACC			1570
TACTCACAGA CGGGATGCTA AGCAGTGCAC CTGCAGTGGT TTAATGGCAG ATAAGCTCCG			1630
TCTGCAGTTC CAGGCCAGCC AGAACTCCT GTGTCCACAT AGAGCTGACG TGAGAAATAT			1690
CTTTCAGCCC AGGAGAGAGG GGTCTGTATC TTAACCCTTT CCTGGGTCTC AGACAACTCA			1750
GAAGGTTGGG GGGATACCAG AGAGGTGGTG GAATAGGACC GCCCCCTCCT TACTTGTGGG			1810
ATCAAATGCT GTAATGGTGG AGGTGTGGGC AGAGGAGGGA GGCAAGTGTC CTTTGAAAGT			1870
TGTGAGAGCT CAGAGTTTCT GGGGTCCTCA TTAGGAGCCC CCATCCCTGT GTTCCCCAAG			1930
AATTCAGAGA ACAGCACTGG GGCTGGAATG ATCTTTAATG GGCCCAAGGC CAACAGGCAT			1990
ATGCCTCACT ACTGCCTGGA GAAGGGAGAG ATTCAGGTCC TCCAGCAGCC TCCCTCACCC			2050
AGTATGTTTT ACAGATTACG GGGGGACCGG GTGAGCCAGT GACCCCTGCG AGCCCCCAGC			2110
TTCAGGCCTC AGTGTCTGCC AGTCAAGCTT CACAGGCATT GTGATGGGGC AGCCTTGGGG			2170
AATATAAAAT TTTGTG			2186

